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OY 301 TPNTFANVTVALSTCTGSGNLODECECELEEFESHNCLTEALIAAKRHSOLFSDQM 360
 DB 361 PPTFAVMAHONENPAVRPOWPVPSLFCSTLPILLLSLM 400
 OY 361 PPTFAVMAHONENPAVRPOWPVPSLFCSTLPILLLSLM 400

RESULT 2
 ID 055243 PRELIMINARY: PRT: 397 AA.

AC 055243:
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
 GN GFR3.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WIDENFALK J., TOMAC A., LINDQVIST E., HOFFER B., OLSON L.
 RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA NAVILHAN P., BAUDET C., MIKAELS O., SHEN L., WESTPHAL H., ENNFORS P.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1997).
 DR EMBL: AF041842; G2921579; -
 DR EMBL: AF036163; G2674177; -
 SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 77.7%; Score 2358; DB 11; Length 397;
 Best Local Similarity 76.8%; Pred. No. 0.00e+00;
 Matches 308; Conservative 56; Mismatches 32; Indels 5; Gaps 4;

DB 1 MGSLERPP--PLMLTLVLVLSM-LPLGANSLATENFVNSCTQARKKCEANPACAKA 57
 OY 1 MWRPLRPRLPVVLMLLLPSPPLPLAAGDLPFESRLMNSCLQARKKCOADPTCSAA 60
 DB 58 YHLSGCTSLSRPLPLESAMSADCLEAAEOLRNSLIDCRCHRRMKHQATCLDIYTWV 117
 OY 61 YHLSGCTSLSRPLPLESAMSADCLEAAEOLRNSLIDCRCHRRMKHQATCLDIYTWV 120
 DB 118 HPARSLGIDYELDVSPYEDVTYSKPMKMLSKLMLKPDSDLCIKFAMLTCLDHCORLTK 177
 OY 121 HRRARSLGIDYELDVSPYEDVTYSKPMKMLSKLMLKPDSDLCIKFAMLTCLDHCORLTK 180
 DB 178 AYGEACSGIRCOHRLCLADLRSEFEKAASHAGLLCCPCPEADACGERRRNTIAPSCA 237
 OY 181 AYGEACSGIRCOHRLCLADLRSEFEKAASHAGLLCCPCPEADACGERRRNTIAPSCA 240
 DB 238 LPSVTNCLDLRSFCRADLRSLDFOHCHPMIDILTCATEOSRCRAVILGLIGTAM 297
 OY 241 LPSVTNCLDLRSFCRADLRSLDFOHCHPMIDILTCATEOSRCRAVILGLIGTAM 300
 DB 298 TPNTFANVTVALSTCTGSGNLODECECELEEFESHNCLTEALIAAKRHSOLFSDQM 357
 OY 301 TPNTFANVTVALSTCTGSGNLODECECELEEFESHNCLTEALIAAKRHSOLFSDQM 360
 DB 358 ADSTSVVOONSAPALRLQPLPILIFS-ILPLILQTLTM 397
 OY 361 PPTFAVMAHONENPAVRPOWPVPSLFCSTLPILLLSLM 400

RESULT 3
 ID 035118 PRELIMINARY: PRT: 397 AA.
 AC 035118:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA 3
 GN (GFRALPHA-3).
 GN GFR3 OR GFRALPHA-3.

OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL6; TISSUE-HEART;
 RX MEDLINE; 98205811.
 RA NOMOTO S., ITO S., YANG L.-X., KIUCHI K.;
 RT "Molecular cloning and expression analysis of GFR alpha-3, a novel
 RT CDNA related to GDNF alpha and NTN alpha."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 244:849-853(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
 RA POESCU N.C., JOHNSON E.M. JR., MILBRANDT J.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
 DR EMBL: AB008833; D1024441; -
 DR EMBL: AF051766; G2961630; -
 DR MGI: 1201403; GFR3.
 SQ SEQUENCE 397 AA; 44307 MW; A80EDD24 CRC32;

Query Match 77.7%; Score 2356; DB 11; Length 397;
 Best Local Similarity 77.9%; Pred. No. 0.00e+00;
 Matches 306; Conservative 53; Mismatches 31; Indels 3; Gaps 3;

DB 7 PPPPLMLLLVLSM-LPLGANSLATENFVNSCTQARKKCEANPACAKA YHLSGCT 65
 OY 9 PLPPVYVLMLLLPSPPLPLAAGDLPFESRLMNSCLQARKKCOADPTCSAA YHLSGCT 68
 DB 66 SLSRPLPLESAMSADCLEAAEOLRNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGD 125
 OY 69 SLSRPLPLESAMSADCLEAAEOLRNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGD 128
 DB 126 YELDVSPYEDVTYSKPMKMLSKLMLKPDSDLCIKFAMLTCLDHCORLTKAYGEACSG 185
 OY 129 YELDVSPYEDVTYSKPMKMLSKLMLKPDSDLCIKFAMLTCLDHCORLTKAYGEACSG 188
 DB 186 IRCQHRLCLADLRSEFEKAASHAGLLCCPCPEADACGERRRNTIAPSCALPSVTPNC 245
 OY 189 IRCQHRLCLADLRSEFEKAASHAGLLCCPCPEADACGERRRNTIAPSCALPSVTPNC 248
 DB 246 LDRSFCRADLRSLDFOHCHPMIDILTCATEOSRCRAVILGLIGTAMTPNTFSKY 308
 OY 249 LDRSFCRADLRSLDFOHCHPMIDILTCATEOSRCRAVILGLIGTAMTPNTFSKY 311
 DB 306 NTVALSTCTGSGNLODECECELEEFESHNCLTEALIAAKRHSOLFSDQMTPNTFSKY 369
 OY 309 NTVALSTCTGSGNLODECECELEEFESHNCLTEALIAAKRHSOLFSDQMTPNTFSKY 372
 DB 366 QOONSAPALRLQPLPILIFS-ILPLILQTLTM 397
 OY 369 QOONSAPALRLQPLPILIFS-ILPLILQTLTM 400

RESULT 4
 ID 035325 PRELIMINARY: PRT: 397 AA.
 AC 035325:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
 GN GFR3.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TRUPP M., RAYNSCHER C., IBANEZ C.F.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF020305; G2429367; -
 SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

Query Match 77.6%; Score 2353; DB 11; Length 397;

248 CLELRRLCFSDPLCRSLRYDFTCHCHPMDI-LGTGATEQ-SRCLRAYLGLIGTAMTPNFA 305
DB 298 DSSSLVAPWCDSCNSGNDLEDLKLNFKNMCKLKNIAQA 339
QY 306 SNVNTSVALLSTCTGRSGNLOECCMELEGFSSHNPCLTEALIA 347

RESULT 7
ID 035748 PRELIMINARY: PRT: 463 AA.
AC 035748:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GDNFR-ALPHA/TRNR1-DELTA PROTEIN.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNAITHI; MORIDAE; MORINAE; RATTUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-HANNOVER;
RA ZHONG J., ANNTES M., HEUMANN R.;
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: A002072; E1154274; -
SQ SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;

Query Match 23.3%; Score 708; DB 11; Length 463;
Best Local Similarity 34.8%; Pred. No. 2,54e-135;
Matches 120; Conservative 74; Mismatches 134; Indels 17; Gaps 14;

DB 1 MFATLTYFALPLDLMSAEVSGDRL-D-CYKASDCLKEGSCSTKYRTLROCVAKET 58
QY 14 VMLLTLPLPPLPLAAGDPLTESRLMNSCLQARRKCOADPTCSAAVHHLDSCSTISST 73
DB 59 NESTLGLLEAKDCRAMEALKOKSLYNGCRKGRKKEKNCRLITYMSQSD-GNDLLE 117
QY 74 PLP-SEEPSVPADCLLAAQOLRNSSLIGCMCHRMNOVACDIYTVHARSGLGYELD 132
DB 118 DSYE-PVNSRLSDIFRAVPEISVEHISGKNCLDAKACNLDITCKKRSAYITPCTTS 176
QY 133 VSEYETVTSKPKM--NLSKLMKL-PSDCLAKFAMCTLNDCKDLKRAKAGECS-G 188
DB 177 MSNEVCNRKCHAKLROFDKVPKASHYGLFCSC--RDIACERRRQITVPCSYERE 234
QY 189 -PH--CORHVCRLRLTLFEKAEPAHAGLLCPCAPNDRGCGERRRNTIAPCALPVA 245
DB 235 RPNCLSLOSCKNTYICRSLADFTNCPESKVSNCLEKENTADLLAYSLGIGVMP 294
QY 246 -PNCLELRRLCFSDPLCRSLRYDFTCHCHPMDI-LGTGATEQ-SRCLRAYLGLIGTAMP 302
DB 295 NYVDSSSLVAPWCDSCNSGNDLEDLKLNFKNMCKLKNIAQA 339
QY 303 SNVNTSVALLSTCTGRSGNLOECCMELEGFSSHNPCLTEALIA 347

RESULT 8
ID 035977 PRELIMINARY: PRT: 464 AA.
AC 035977:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GN GDNFR-BETA OR RETL2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNAITHI; MORIDAE; MORINAE; RATTUS.
RN (1)
RP SEQUENCE FROM N.A.
RC TRUPP M., RAYNOSCHER C., IBANEZ C.F.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RX MEDLINE; 9732356.

RA SANICOLA M., HESSION C.A., WORLEY D.S., CAMILLO P., EHRENFELS C.,
RA WALDS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PEPINSKY R.B., CATE R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation
can be mediated by two different cell-surface accessory proteins."
RL PROC. NATL. ACADE. SCI. U.S.A. 94:6238-6243(1997).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RA SANICOLA M., HESSION C.A., WORLEY D.S., CAMILLO P., EHRENFELS C.,
RA WALDS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PEPINSKY R.B., CATE R.L.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF005226; G2232252; -
SQ SEQUENCE 464 AA; 51668 MW; B1A2BD11 CRC32;

Query Match 23.2%; Score 704; DB 11; Length 464;
Best Local Similarity 35.3%; Pred. No. 2,33e-134;
Matches 121; Conservative 87; Mismatches 108; Indels 27; Gaps 14;

DB 21 ASPSSLOGE-LHG-WRPQVDCVRANELCAEESNSSRYTLROCLAG-RDK-NIHLAA-
QY 23 PSLPLAAGDPLTESRLMNSCLQARRKCOADPTCSAAVHHLDSCSTISSTPLSEFEPV 73
DB 76 -KECOALEVLOESPLYDCRCRKGKKELOCLOIYWSHGLTGE-EFEYASPEPVTS 132
QY 83 PADCLLAAQOLNSSLIGCMCHRMNOVACDIYTVHARSGLGYELD-DSPHYIV 132
DB 134 RLSDIFRLASIFSGTGTPAVSTKSNHCLDAKACNLDNCKKRLSSYSISCNREISPM 134
QY 142 --SKWKM-NL-S-K-LN-MLKPSDCLKFMCTLNDCKDLKRAKAGECS--G 134
DB 194 KCRNRKCHAKLROFDKVPKASHYGLFCSC--QDQAEERRQITVPCSYERE 234
QY 190 HCRVVCRLRLTLFEKAEPAHAGLLCPCAPNDRGCGERRRNTIAPCALPVA-PNC 245
DB 252 LDRSLCRTLDCRSLRADFNACRASRYRTTSCPADVYQCLGSYACMIGEDMTPNVD 311
QY 249 LELRLCFSDPLCRSLRYDFTCHCHPM-DIIGTCATEQSR-CLRAYLGLIGTAMTPNFA 306
DB 312 SNPTGIVSPMCGNSGMECEKFLRDEFTENCLKNIAQA 354
QY 307 NVNTSVALLS-CTGRSGNLOECCMELEGFSSHNPCLTEALIA 347

RESULT 9
ID 015316 PRELIMINARY: PRT: 464 AA.
AC 015316:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
GN GDNFR-BETA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-FETAL BRAIN;
RA MARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M.,
RA MOSHNAKOV M., AIKASINEN M.S., PALOTIE A., SARIOA H., SAARMA M.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U93703; G2228737; -
SQ SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;

Query Match 23.1%; Score 701; DB 4; Length 464;
Best Local Similarity 35.7%; Pred. No. 1,23e-133;
Matches 115; Conservative 87; Mismatches 95; Indels 25; Gaps 18;

DB 40 CVRANELCAEESNSSRYTLROCLAG-RDR-NITMLAN--KECOALEVLOESPLYDCRC 95
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ORIGIN

Query Match 60.28; Score 1199; DB 27; Length 1203;
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 QY 323 ATGAACAGCTGTCTCCAGCGCAGAGAGAGTGCAGGCTGATCCACCTGCACTGCTGCC 382
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 Db 181 TACCACACCTGATTCCTGACCTCTAGCATAAAGCAGCCGCACTGCGCTCAGAGAGAGCT 240
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 QY 383 TACCACACCTGATTCCTGACCTCTAGCATAAAGCAGCCGCACTGCGCTCAGAGAGAGCT 442
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 QY 503 TGCATGTGCCACCGCGCGCATGTGSAACAGAGTTCCTGCTGATGATCTATAGAGCCGTT 562
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 Db 361 CACCGTCCCGGAGCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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 QY 563 CACCGTCCCGGAGCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
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 Db 421 ACCGAAACCTTGAAATGATCTCAGCAAACTGCAAACTGCTCAAAACAGACTCAGAC 480
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 QY 623 ACCGAAACCTTGAAATGATCTCAGCAAACTGCAAACTGCTCAAAACAGACTCAGAC 682
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 Db 481 CTCTGCTCAAGTTGGCATGTGTGATCTCAATGACAAGTGTGACCGGTGCGCAG 540
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 QY 683 CTCTGCTCAAGTTGGCATGTGTGATCTCAATGACAAGTGTGACCGGTGCGCAG 742
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 Db 541 GCGTAGCGGAGCGCTGCTCGGCGCCCATGTCAGCGGCAAGCTGCGCTCAGGAGCGTG 600
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 Db 601 CTCTACTTTCTTCAGAGAGCGCGGAGCGCCAGCGCAGGCGCTGCTACTGTGCCATGT 660
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 QY 803 CTCTACTTTCTTCAGAGAGCGCGGAGCGCCAGCGGCGCTGCTACTGTGCCATGT 862
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 Db 661 GCCCCCAAGCAGCGGGGCTCGGGGAGCGCGCGGCAACCATGCGCCCAACTGCGCG 720
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 Db 721 CTGCGCGCTGTGGCGCCCACTGCTGAGACTGCGGGGCTGCTGCTTCCGACCGGCTT 780
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 QY 923 CTGCGCGCTGTGGCGCCCACTGCTGAGACTGCGGGGCTGCTGCTTCCGACCGGCTT 982
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 Db 781 TGCAGATCAGCGCTGTGATTTCCAGACCCAGCTGCAATGCCATGAGCATCTAGAGAACT 840
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 Db 1081 CCACACCTTACCTTCTGATGAGCAGCAGAGTGAAGAAACCTGCTGTGAGGCACTA 1140
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RESULT 2
 LOCUS AB008833 1867 bp mRNA ROD 23-Apr-1999
 DEFINITION Mus musculus mRNA for Gfralpha-3, complete cds.
 ACCESSION AB008833
 NID 92627159
 KEYWORDS Gfralpha-3.
 SOURCE Mus musculus (strain: C57BL/6) adult heart cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Nomoto, S., Ito, S., Yang, L. X., and Kiuchi, K.
 TITLE Molecular cloning and expression analysis of GFR alpha-3, a
 CDNA related to GDNF alpha and NTN alpha
 JOURNAL Biochem. Biophys. Res. Commun. 244 (3), 849-853 (1998)
 MEDLINE 98205811
 REFERENCE
 AUTHORS Nomoto, S.
 TITLE 2 (bases 1 to 1867)
 JOURNAL Direct Submission
 Submitted (13-NOV-1997) to the DDBJ/EMBL/GenBank databases. Satoshi
 Nomoto, RIKEN (The Institute of Physical and Chemical Research),
 Bio-Mimetic Control Research Center; 2271-130 Anagahora,
 Shimoshidami, Moriyama-ku, Nagoya, Aichi 463, Japan
 (E-mail: nomoto@nagoya.riken.go.jp, Tel: 81-52-736-5864,
 Fax: 81-52-736-5865)

FEATURES
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 Location/Qualifiers
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Db	215	CCGCGTTGCAAGG	TGCTCTACAGAC	ACTGGGCTCTGCGACCTCCAGTTT	TAAGAGCGCC	274
Qy	365	CCCACTCTGCAATG	TGCTGCTACCAACAC	CTGAAATCTCTGCACTTAAGATTA	GAACACCCA	424
Db	275	CTGCCCTTAAGAG	AGTGGCTGCCATG	TTCGACAGACTG	CTTAAGGACGCAAAACTAGG	334
Qy	425	CTGCGCTCAGAGG	AGCCTTGGTGTCCCTG	CTGACTGCTGGAGGCGACACAACT	CACTAGG	484
Db	335	AACAGCTCTCGAT	AGACTGCAAGTGCAT	TGGCGCATGGAACACCAACT	CACTGCTG	394
Qy	485	AACAGCTCTCGAT	AGACTGCAATG	CTCATGCTCCACCGCGCATTAAGAAAC	CAAGTTCCTGCTG	544
Db	395	GACATTTATTTG	AGACCTGTTCAC	CCCTGCCAGGCTTGGT	GTGACTACGAATGGATGTCTCA	454
Qy	545	GACATCTATTTG	AGACCTGTTCAC	CCGCTGCCAGGCTTGGTAACTAAGACT	CGATGTCTCC	604
Db	455	CCCTATGAAGAC	AGTGAACAGAAACCT	GTGAAAAATGAATCTTAAGAAAGTGAACATG	514	
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Qy	665	CTCAAAACAGACT	GAAGCTGTGCTCTCAAAATTTG	CTATGCTGTACTCTTCAATGACAG	724	
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Db	935	CTGATTTGGAG	CTGCCATACCCCAAACTTCA	TCAAGCAAGGTCAACACTACTGTGCTTA	994	
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Db	995	AGCTGACACT	GCCGAGGACGGGCAACT	TACAGACAGATGTAAACAGCTGGAAAGTCC	1054	
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Db	1055	TTCTCCACAAC	CCCTGCGCTGTGGAGGCAAT	TGCACATAGATGTGTTTCCACAGACAG	1114	144
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Db	1175	CCGTGCTCAG	AGCTGGAGCCAGGCTAT	CAATCTTTCTTCTTCAATCTTCCCTTGAT	1234	
Qy	1325	CTGTGCTGTAG	GGCCACAGCCCTGGGGT	GGCCTCTCTTTTCTCTGACAGGCTTCCCTTGAT	1384	

D	1235	CTGTGCAGACCCCTCTGGTAGCTGGGCTTCTTCAGGGCTCTTTTGCTCTTCACACACC	1294
O	1385	CTGCTCGACCACTATGATGACTGGACTTCCCCAGGGGCCCTCT-TCCCCTTCACACACC	1443
D	1295	CAGACTGATTGGCAGCCCTGTGGTGGAGAGAACAATCGCAGCCTGTGGGAAGAAGCGCAC	1354
O	1444	CAGGTGAGCTTCAGACCCACAAAGGGGTGTAGGAAAGACAGCAGCAGGAAGAGGTGCAGT	1503
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R	RESULT	5	
L	LOCUS	MTRNR3	1932 bp mRNA ROD 03-MAR-1994
D	DEFINITION	Mus musculus mRNA for TGF-beta-related neurotrophic factor	
A	ACCESSION	Y15110	
N	KEYWORDS	neurotrophic receptor; TGF-beta related protein; trnr-3 gene	
S	SOURCE	house mouse.	
O	ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euhit:	
R	REFERENCE	1 (bases 1 to 1932)	
A	AUTHORS	Zhong,J., Anlies,M., Tolle,A. and Heumann,R.	
T	TITLE	Molecular cloning of a new member of trnr family	
J	JOURNAL	Unpublished	
R	REFERENCE	2 (bases 1 to 1932)	
A	AUTHORS	Zhong,J.	
T	TITLE	Direct Submission	
J	JOURNAL	Submitted (14-OCT-1997) J. Zhong, Molecular Neurobiochemistry,	
		NCI/1172, Ruhr-University Bochum, universitaetsstr. 150, D-46206	
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C	COMMENT	Related publication: Lennon G. et al, Genomics 33, 151-155.	
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		YLGIETGATPNFISKVNTVALSTCTGSGSGNLDOECDELERSFSONCLVEAIIAA*	
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O	ORIGIN		
Q	Query Match	40.5%; Score 807; DB 29; Length 1932;	
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D	175	GCACAGAGAAAGGTTTGGAGACAGCTGACCCAGGCGCAGAAATAATCGAGGCTAAT	234
O	305	CCACAGAAAAGCCGACTCATGAAACAGCTGTCTCCAGGCCAGAGAGAAAGTCCAGGCTGAT	364

D	235	CCGGCTTGC	AAGGCTG	CCCTAC	AGCACT	GGGCTCT	GTG	CACTCA	AGTTTAA	GCGGCCG	294		
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D	535	CTCAACAC	GAGACT	GGAGC	CTT	GGGCTCA	AAATTTG	CTATG	CGTGT	ACTCTTCA	CGACAG	594	
O	665	CTCAACAC	GAGACT	GGAGC	CTT	GGGCTCA	AAATTTG	CTATG	CGTGT	ACTCTTCA	CGACAG	724	
D	555	TGTGAC	CGGCTG	CGCA	AGGCTTAC	GGGAGG	CACTG	CAAGGAT	CCGCTT	CCAGCCAC	654		
O	725	TGTGAC	CGGCTG	CGCA	AGGCTTAC	GGGAGG	CACTG	CAAGGAT	CCGCTT	CCAGCCAC	784		
D	655	CTGTG	CCCTA	AGCCAG	CTG	CGCTCTT	TTTG	AAGAGC	ACAGAGT	CCACGCTCA	AGGCT	714	
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D	715	CTGTG	CTGT	TCCCTG	CTCA	CAAGAGAT	ATG	CGGGGCTGT	GGGAGG	CGGCGGCTTA	CACC	774	
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RESULT 7
LOCUS AF041842 1244 bp mRNA ROD 16-JUN-1998
DEFINITION Mus musculus glial cell line-derived neurotrophic factor family
receptor alpha-3 (gfra3) mRNA, complete cds.
ACCESSION AF041842

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NID 92921578
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sclerognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1244)
AUTHORS Widenfalk, J., Tomac, A., Lindqvist, E., Hoffer, B. and Olson, L.
TITLE GFRA1pha-3, a protein related to GFRA1pha-1, is expressed in
developing peripheral neurons and ensheathing cells
JOURNAL Eur. J. Neurosci. 10 (4), 1508-1517 (1998)
MEDLINE 98420233
REFERENCE 2 (bases 1 to 1244)
AUTHORS Tomac, A., Hoffer, B. and Olson, L.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-1998) Neuroscience, Karolinska Institute,
Doktorarlingen 12, Stockholm 17177, Sweden
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RESULT 8 HUM2D48G06 521 bp mRNA PRI 29-AUG-1998
LOCUS Homo sapiens full length insert cDNA clone ZD48G06.
ACCESSION AF086292
NID 93483637
KEYWORDS FLI_CDNA.
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE 1 (bases 1 to 521)
AUTHORS Moesner,J., Tan,F., Marra,M., Kucab,T., Yandell,M., Martin,J.,
        Martin,G., Bowles,L., Wylie,T., Bowers,T., Stepoe,M., Theising,B.,
        Gelsel,S., Allen,M., Underwood,K., Chappell,J., Pearson,B.,
        Gidbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
        Schurk,R., Ritzer,E., Kohn,S., Swaller,T., Behmer,K., Hillier,L.,
        Wilson,R. and Waterston,R.
        Full Clone Sequencing of the Longest Available Member from Each
        Unigene Cluster

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 521)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington
        University, 4444 Forest Park Avenue, St. Louis, Missouri 63110
SUBMITTED BY:
        Genome Sequencing Center
        Department of Genetics
        Washington University
        St. Louis MO 63108 USA
        http://genome.wustl.edu/gsc
        mailto:est@wustl.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA.
        attempt has been made to verify whether this corresponds to a
        full-length of the original mRNA from which it was derived. It
        have tried to obtain double-stranded, or double chemistry
        across the entire clone, but potentially, there are areas in the
        sequence where this level of coverage was not achieved.
        Nevertheless, we are confident of the accuracy of this sequence
        all regions of low quality, as defined by PHRAP (P. Green, in
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BASE COUNT 111 a 147 c 120 g 143 t
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        Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS	9	HMMZD48G06	521 bp	mRNA	PRI	29-AUG-1998
DEFINITION		Homo sapiens full length insert cDNA clone ZD48G06.				
ACCESSION		AF086292				
NID		g3483637				
KEYWORDS		FLI CDNA.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
AUTHORS		Primates; Catarrhini; Hominiidae; Homo.				
TITLE		1 (bases 1 to 521)				
JOURNAL		Messenger J., Tan, F., Marra, M., Kucaba, T., Yangel, M., Martin, J.,				
REFERENCE		Wessinger, J., Allen, M., Underwood, K., Chappell, J., Person, B.,				
AUTHORS		Gelbois, S., Bowles, L., Wylie, T., Bowers, Y., Steptoe, N., Thelsing, B.,				
TITLE		Claiborn, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R.,				
JOURNAL		Schurt, R., Ritter, E., Kohn, S., Swaller, T., Behmyer, K., Hillier, L.,				
COMMENT		Wilson, R. and Waterston, R. Full Clone Sequencing of the Longest Available Member from Each Unigene Cluster Unpublished 2 (bases 1 to 521) Waterston, R. Direct Submission Submitted (24-AUG-1998) Department of Genetics' Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA SUBMITTED BY: Genome Sequencing Center Department of Genetics Washington University St. Louis MO 63108, USA http://genome.wustl.edu/gsc mailto:est@watson.wustl.edu				

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

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FEATURES             location of this clone is unknown.
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Best Local Similarity 97.1%; Pred. No. 2,82e-97;
Matches 168; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
339 CCCCCTGCCTCCTCTGTGATGGAGGATGCAAAACAACCTGCTGCACTGCCCTTCCCG 398
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CP   173 CCCCTCCG-CCTCTCCCTCCGATGGAGATGCAAAACTACTGCTGCTGCACTGCCCTTCCCG 115
Db   399 GGATCTCGCGCAACATCTGGGCGCATAGAAGCGTGGAAGCGCTGSGGCTTGATTTCCTA 458
CP   114 GGATCTCGCGCAACATCTGGGCGCATAGAAGCGTGGAAGCGCTGSGGCTTGATTTCCTA 55
Db   459 TTATGTCTTAAGTCTCTGTGGGCTTGTGATTCATGATTAACCTTTGACTT 511
CP   54  TTATGTCTTAAGTCTCTGTGGGCTTGTGATTCATGATTAACCTTTGACTT 2
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LOCUS	166494	7218 bp	DNA	PAT	23-DEC-1997
DEFINITION	Sequence 14 from patent US 5670367.				
ACCESSION	166494				
NID	92724471				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 7218)				
AUTHORS	Dorner, F., Schellinger, F. and Falkner, F. Gunter.				
TITLE	Recombinant fowlpox virus				
JOURNAL	Patent: US 5670367-A 14 23-SEP-1997;				
FEATURES	Location/Qualifiers				
source	1..7218				
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Db 1147	yy				
Qy 1601	tgtctgccctctgtgtgcacacatttagcagatgtatctggtggtgacacagctc				
Db 1207	yy				
Qy 1661	aagccctcttgagaccctctctctgactaccagatcacacagatctaatat				
Db 1267	yy				
Qy 1721	ctttcttattgcattccagattagcggttagggagagactgggtgtctgaaac				
Db 1327	yy				
Qy 1781	cttgaagagcattctcctttgtgaagagctctgcccctctctctctctctct				
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Qy 1841	ggagatggaatactactgctgacactccctgctcccgatcctgccgaac				
RESULT 11					
LOCUS	AB008833	1867 bp	mRNA	ROD	23-APR-1997
DEFINITION	Mus musculus mRNA for GFRalpha-3, complete cds.				
ACCESSION	AB008833				
NID	92627159				
KEYWORDS	GFRalpha-3				
SOURCE	Mus musculus (strain: C57BL/6) adult heart cDNA to mRNA.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
AUTHORS	Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (sites)				
JOURNAL	Nemoto, S., Ito, S., Yang, L. X. and Kiuchi, K.				
MEDLINE	Molecular cloning and expression analysis of GFR alpha-3, a novel				
REFERENCE	cDNA related to GDNF alpha and NTN alpha				
AUTHORS	Biochem. Biophys. Res. Commun. 244 (3), 849-853 (1998)				
TITLE	98205811				
JOURNAL	2 (bases 1 to 1867)				
DEFINITION	Nemoto, S.				
ACCESSION	Submitted (13-NOV-1997) to the DDBJ/EMBL/GenBank databases. Satoh, T.				
NID	Nemoto, RIKEN (The Institute of Physical and Chemical Research),				
KEYWORDS	Bio-Mimetic Control Research Center; 2271-130 Akiyoshi, S.				
SOURCE	Shimoshidani, Moriyama, Ku, Nagoya, Aichi 463, Japan				
ORGANISM	(E-mail: nemoto@nagoya.riken.go.jp, Tel: 81-52-736-5864,				
REFERENCE	Fax: 81-52-736-5865)				
AUTHORS	Location/Qualifiers				

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BASE COUNT 384 a 572 c 474 g 437 t

ORIGIN

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Matches 75; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Cp 44 AAAGTCTCTCGGCTGTGATCATGATTAACCTT 7
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RESULT 12
LOCUS AF051766 1884 bp mRNA ROD 26-JUN-1998
DEFINITION Mus musculus GDNF family receptor alpha 3 mRNA, complete cds.
ACCESSION AF051766
MID g2961629
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1884)
AUTHORS Baloh,R.H., Gorodlinsky,A., Golden,J.P., Tansey,M.G., Keck,C.L.,
Popescu,N.C., Johnson,E.M. Jr. and Milderand,J.
TITLE GfRalpha3 is an orphan member of the GDNF/neurturin/persephin
receptor family
JOURNAL Proc Natl. Acad. Sci. U.S.A. 95 (10), 5801-5806 (1998)
MEDLINE 98245162
AUTHORS 2 (bases 1 to 1884)
TITLE Baloh,R.H. and Milderand,J.D.
JOURNAL Direct Submission
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Location/Qualifiers
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63. .1256
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Best Local Similarity	76.5%:	Pred. No.	3.50e-16;		
Matches	75;	Conservative	0;	Mismatches 23;	Indels 0; Gaps 0;
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DEFINITION	Mus musculus mRNA for TGF-beta-related neurotrophic factor receptor-3.				
ACCESION	NID	g285985			
KEYWORDS	neurotrophic receptor; TGF-beta related protein; trnr-3 gene.				
SOURCE	house mouse.				
ORGANISM	Mus musculus. Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	AUTHORS Zhong,J., Anlies,M., Tolle,A. and Heumann,R. TITLE Molecular cloning of a new member of TrnR family JOURNAL Unpublished REFERENCE 2 (bases 1 to 1932) AUTHORS Zhong,J. DIRECT Submision SUBMITTED (14-OCT-1997) J. Zhong, Molecular Neurobioclin, NCI/112, Ruhr-University Bochum, Universitaetstr. 150, D-4 Bochum, FRG				
COMMENT	Related publication: Lennon G. et al, Genomics 33, 151-153, 1997.				
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BASE COUNT	414 a	586 c	491 g	441 t	
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polya_site
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BASE COUNT 384 a 572 c 474 g 437 t

ORIGIN

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Q	y	200	GAAGAAGATGGAGGCTAATCCGCGCTTGCAAGGCTGCTACACAGCACTGGGCTTCCTGCA	259
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Q	y	260	CCCCAGCTCAGAGAGTCCATGCTGCTCAGGGAGTCTGCCACATCTGCACTGCTGCTTG	319
D	b	299	AGGCAGAGAACTAGAGAACTGCTCTGATAGACTGCAAGTGCATCGCGCATGA	358
Q	y	320	AAGCAGCAGCACTAGAGAACTGCTCTGATAGACTGCAAGTGCATCGCGCATGA	379
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D	b	419	ACTAGAGTTGATGTCTCAACCTATGAAGACAGTGAACAGCAACCTGGAAATGA	478
Q	y	440	ACTAGAGTTGATGTCTCAACCTATGAAGACAGTGAACAGCAACCTGGAAATGA	499
D	b	479	ATCTTGAAGTTGAACTGTAACATGCTCAAAACAGACTGCGACTGTGCTTAAATTTGCTATGC	538
y		500	ATCTTGAAGTTGAACTGTAACATGCTCAAAACAGACTGCGACTGTGCTTAAATTTGCTATGC	559
D	b	539	TGTGTACTCTTCAACAGCAATGTGACCGCTGCGCAAGGCTTACGGGGAGCATGCTCAG	598
Q	y	560	TGTGTACTCTTCAACAGCAATGTGACCGCTGCGCAAGGCTTACGGGGAGCATGCTCAG	619
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Q	y	620	GGATCGCGCTGCAAGCGGCACCTGCTGCTTACCCAGCGGCGCTCTTCTTGAAGAAGCAG	679
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Q	y	800	GGCTGATCTTGGGACCTTCTGCGTGGGAGACCTTGTGACATACGCTGTATGACT	859
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DB 1335 GCTGGCGCTGTGAGAGAGAGAGCGGCTGTACACAGCA 1372

RESULT 5
LOCUS AF041842 1244 bp mRNA 16-JUN-1998
DEFINITION Mus musculus glial cell line-derived neurotrophic factor family
ACCESSION AF041842
NID 92921578
KEYWORDS house mouse,
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1244)
AUTHORS Widenfalk, J., Tomac, A., Lindqvist, E., Hoffer, B. and Olson, L.
TITLE GFRA1pha-3, a protein related to GFRA1pha-1, is expressed in developing peripheral neurons and ensheathing cells
JOURNAL Eur. J. Neurosci. 10 (4), 1508-1517 (1998)
MEDLINE 98420233
REFERENCE 2 (bases 1 to 1244)
AUTHORS Tomac, A., Hoffer, B. and Olson, L.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-1998) Neuroscience, Karolinska Institute, Doktorstingen 12, Stockholm 17171, Sweden
FEATURES
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51..1244
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/db_xref="pid:g2921579"
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KEAMCTLDKCDRLKRAYEAGSGIRICORHLQALRSFEKAAESHAQGLLPCP
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 TCATEOSRCLRAYLIGTAMTNPFIISKVTNTVALSCTGSGNINODEOEOLERSFSO
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 LOTLW

BASE COUNT 259 a 394 c 325 g 266 t
 ORIGIN

Query Match 61.1% Score 1038: DB 29: Length 1244:
 Best Local Similarity 92.3% Pred. No. 0.00e+00;
 Matches 1149: Conservative 0; Mismatches 93; Indels 3; Gaps 2;

2 CGGCGCCCAAGC-AGGAGAGCGCTGTCCATCCGCGGCTTCA--CCGCGCATGGGGCT 58
 15 CGAGCGCCAGACAGAGAGCGCTGCGGGGCTCGAGACCGCGCATGGGGCT 74
 59 CTCCCTGGAGCCCGACCTCACTGCTGATGATCTGCTGCTGCTGCTGCTGCTGCT 118
 75 CTCCCGGAGCCCGACCGCGCGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 134
 119 GCCACTTGGAGAGAACTCCCTGCGACAGAGAAAGGTTGTGAACGCTGTACCA 178
 135 ACCCTTGGAGAGAACTCCCTGCGACAGAGAAAGGTTGTGAACGCTGTACCA 194
 179 GGGCAGAAAGAAATGGAGGCTAATCCGCTTGCAGAGGCTGCTTACAGACCTGGGCT 238
 195 GGGCAGAAAGAAATGGAGGCTAATCCGCTTGCAGAGGCTGCTTACAGACCTGGGCT 254
 239 CTGCACTCTCACTTTAAGCAGCGCGCTGCTTGAAGAGTGTGCTGCTGCTGCTGCT 298
 255 CTGCACTCTCACTTTAAGCAGCGCGCTGCTTGAAGAGTGTGCTGCTGCTGCTGCT 314
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 315 CCTGAGAGAGAGAGAACTGCTGAGAAAGCTGCTGATGAGTGTGAGTGGCATGGGCT 374
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 375 CATGAAGCAGCAAGTACCTGTCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 434
 419 TGGTGAAGCAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 478
 435 TGGTGAAGCAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 494
 479 AATGAATCTTACAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 538
 495 AATGAATCTTACAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 554
 539 TATGCTGTACTCTTACAGAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 598
 555 TATGCTGTACTCTTACAGAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 614
 599 CTCAGAGATCCGCTGCGACGCTGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 658
 615 CTCAGAGATCCGCTGCGACGCTGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 674
 659 GGCAGAGAGTCCAGAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 718
 675 GGCAGAGAGTCCAGAGTGTGATGCTGCTGAGCAATTTATGGACGCTTACCTGCGCGAAGCT 734
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 779 CAATTGCTGATCTGCGGAGTGTGCGGTGCGGAGCTTGTGTGATGATGAGTGGCTGAT 838
 795 CAATTGCTGATCTGCGGAGTGTGCGGTGCGGAGCTTGTGTGATGATGAGTGGCTGAT 854
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QY 915 CAGATGTCTGGGCGATACCTGCGGCTAATTTGAGCTGCGCATGACCCCAACTTATCAG 974
 DB 959 CAAGGTCAACACTACTGTTGCTTAACTGACCTGCGGAGCGAGCGGCACTACAGGA 1018
 QY 975 CAAGGTCAACACTACTGTTGCTTAACTGACCTGCGGAGCGAGCGGCACTACAGGA 1034
 DB 1019 CGAGGTGAACAGCTGGAAGGCTTCTTCCAGAAACCCCTGCTGTGAGAGCCATTG 1078
 QY 1035 CGAGGTGAACAGCTGGAAGGCTTCTTCCAGAAACCCCTGCTGTGAGAGCCATTG 1094
 DB 1079 AGCTAAGATCGCTTCCAGAGAGCTTCTTCCAGAGAGCTGCGGAGACTACTTTTC 1138
 QY 1095 GGTAAATGCGTTTCCAGAGAGCTTCTTCCAGAGAGCTGCGGAGACTACTTTTC 1158
 DB 1139 AGTGTGAG 1198
 QY 1155 TGTGATGAG 1218
 DB 1199 TTTCTTCTCCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1243
 QY 1215 GTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1259

RESULT 6
 LOCUS AF020305 1194 bp mRNA 23-SEP-1997
 DEFINITION Mus musculus glial cell line-derived neurotrophic factor family
 receptor alpha-3 (gfra-3) mRNA, complete cds.
 ACCESSION AF020305
 NID 92429366
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eulalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 1194)
 Trupp, M., Raynoschek, C. and Ibanez, C.F.
 Multiple G-protein-coupled receptors control GDNF-dependent and independent activation of the c-ret receptor tyrosine kinase.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1194)
 Trupp, M. and Ibanez, C.F.
 Direct Submission
 TITLE Submitted (20-AUG-1997) Neuroscience, Karolinska Institute, Doktorsringen 12A, Stockholm 17177, Sweden
 JOURNAL
 FEATRES
 source
 1. 1194
 Location/Qualifiers
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 /db_xref="taxon:10090"
 1. 1194
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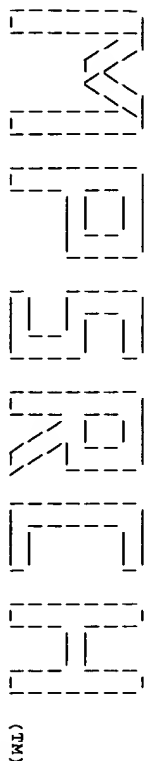
BASE COUNT 253 a 372 c 307 g 262 t
 ORIGIN
 Query Match 60.4% Score 1027: DB 29: Length 1194:
 Best Local Similarity 93.0% Pred. No. 0.00e+00;

Db 149 DPATSKSNHCLDAAKACNLNDKCRKLSRGVLSNCSMEIATSEHCSRCKHKLRFQFDN 208
Oy 153 KP--DS--DLCLFRMLCTLMDKCDRLKAIGKACS--GI-----RCORHLLDLAORISFEK 203
Db 209 VPSEVYTRLLFCSCSK--DOA--CAEPRTOTVPFCSYEDKEKPKNCIDLNNVCRADHLCSRL 266
Oy 204 AAESHAAQGLLLCPACBEPADGEGERRRNTIAPSCALPSVA--PNCULNLSFCRAPPLCSRL 262
Db 267 ADFHANCQASQSLTSCSGDNVQACLSYGLISFDMTPTNYVDASTSTIISPMSCCKGS 326
Oy 263 MDFQTHCP--MDILGTCACTEGRS--CLRAYLGLIGTAMTPNFIKSVNTVAIG--CTCRGS 318
Db 337 GNLEEECEKFLDFETNCLNAIAQA 352
Oy 319 GNLODECEQLEKSFSONPCLMEALIAA 344

RESULT	2	STANDARD:	PRT:	463 AA.
AD	NTRR_MOUSE			
AC	008842:			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	NEUTROTIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (TGF-			
DE	BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GNF RECEPTOR BETA)			
DE	(GNFR-BETA).			
GN	GNFR2 OR GDNFRB OR TRNR2.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:			
OC	EUTHERIA: RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97325791.			
RA	BALOH R.H., TANSEY M.C., GOLDEN J.P., CREEDON D.J.,			
RA	HEUCEROH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,			
RA	JOHNSON E.M. JR., MILBRANDT J.,			
RL	NEURON 18:793-802(1997).			
CC	-1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED			
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE			
CC	TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE			
CC	RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY			
CC	SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CEREBRAL AND DORSAL			
CC	ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN			
CC	AND IN THE ADRENAL.			
CC	-1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE			
CC	SPLICING.			
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.			
DR	EMBL: AF002701; G2145082; -			
DR	MED: MGI:1195462; GFR2.			
KM	RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;			
KM	ALTERNATIVE SPLICING.			
FT	SIGNAL	1	21	
FT	CHAIN	22	443	
FT	PROPEP	444	463	
FT	CARBOHYD	52	52	POTENTIAL.
FT	CARBOHYD	357	357	TGF-BETA RELATED NEUROTROPHIC FACTOR
FT	CARBOHYD	413	413	RECEPTOR 2.
FT	LIPID	443	443	HYDROPHOBIC, REMOVED DURING MATURATION
FT	VARSLIC	14	146	(POTENTIAL).
SO	SEQUENCE	463 AA;	51598 MW;	POTENTIAL.
			0A2165C0 CRC32;	
	Query Match	25.78;	Score 762;	DB 1; Length 463;
	Best Local Similarity	37.94;	Pied. No. 1,00e-163;	
	Matches 122; Conservative	75;	Mismatches 100;	Indels 25; Gaps 1
DB	40 CVRANELCAEISCSRSRYRLRQC--LAGR-DRNTMLNKEQQAALVLYDSPLYDRC 95			
	: : : : : : : : : : : : : : : : : : :			
Y	41 CTQARKKCEANPCAKAYOHLSCTPSLSPGSGSATSAACLEAQQLRNSSLTIDRC 100			

[illegible]

RESULT	3	STANDARD:	PRT:	464 AA.
ID	NRTR_HUMAN			
AC	000451;			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	NEURURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (TGFBETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GNFR RECEPTOR BETA)			
DE	(GNFR-BETA).			
GN	GFRA2 OR GNFRB OR TRNR2.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE; 97325791.			
RA	BALLO R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,			
RA	JOHNSON E.T.H., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,			
RA	NEURON 18:793-802(1997).			
RL				
CC	-1- FUNCTION: RECEPTOR FOR NEURURIN. MEDIATES THE NRN-INDUCED			
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE			
CC	TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE			
CC	RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY			
CC	SIMILARITY).			
CC	-1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE			
CC	SPLICING IN BOTH BRAIN AND PLACENTA.			
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.			
DR	EMBL; AF002700; G2145080; -.			
DR	MTM; 601956; -.			
KW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;			
KW	ALTERNATIVE SPLICING.			
FT	FT SIGNAL	1	21	POTENTIAL.
FT	FT CHAIN	22	444	TGF-BETA RELATED NEUROTROPHIC FACTOR
FT	FT PROPEP	445	464	RECEPTOR 2. HYDROPHOBIC, REMOVED DURING MATURATION
FT	FT CARBOHYD	52	52	(POTENTIAL).
FT	FT CARBOHYD	357	357	POTENTIAL.
FT	FT CARBOHYD	413	413	POTENTIAL.
FT	FT LIPID	444	444	GPI-ANCHOR (POTENTIAL).
FT	FT VARSPLIC	14	146	MISSING (IN SHORT FORM).
SO	SEQUENCE	464 AA;	51558 MM;	3C7ABBF8 CAC32;
Query Match		25.6%;	Score 759;	DB 1; Length 464;
Best local Similarity		37.3%;	Pred. No. 6.34e-163;	
Matches 120;	Conservative	78;	Mismatches 99;	Indels 25; Gaps 18
db	40 CVANMELCAEBSGSSRYRTLRQC---LAGR-DRTNMLANKKECOALAEVLOESPLYDCRG 9"			



(TM)

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:07:03 1999; Maspar time 36.88 Seconds

Tabular output not generated. 694.165 Million cell updates/sec

Title: >US-08-866-354-36
Description: (1-464) from US08866354.pep
Sequence: 3386
1 MILANVFCLFFFLDITLRL.....RAPSALTIVSLMKLAL 464

Scoring table:
PAM 150
Gap 11

Searched: 180763 seqs, 55169189 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl8
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 46.920; Variance 70.591; scale 0.665

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3383	99.9	464	4	RET LIGAND 2.	0.00e+00
2	3383	99.4	464	4	GLIAL CELL LINE-DERIVE	0.00e+00
3	3332	95.5	464	11	GLIAL CELL LINE-DERIVE	0.00e+00
4	1535	45.3	464	11	GNFR-ALPHA/TRNR1-DELT	0.00e+00
5	1527	45.1	468	11	GNFR RECEPTOR ALPHA	0.00e+00
6	1520	44.9	465	4	GNFR-RELATED ANCHOR PROT	0.00e+00
7	1508	44.5	463	11	GNFR RECEPTOR BETA	0.00e+00
8	1499	44.3	460	4	RET LIGAND 1.	0.00e+00
9	1392	41.1	431	13	GNFR RECEPTOR ALPHA 4 P	0.00e+00
10	782	23.1	397	11	GLIAL CELL LINE-DERIVE	6.73e-172
11	782	23.1	397	11	GLIAL CELL LINE-DERIVE	6.73e-172
12	782	23.1	397	11	GLIAL CELL LINE-DERIVE	6.73e-172
13	705	20.8	400	4	GNFR FAMILY RECEPTOR A	5.00e-151
14	107	3.2	1713	11	LATEIN TGF BETA BINDIN	6.41e-03
15	110	3.2	2090	5	CODED FOR BY C. ELEGAN	1.98e-03
16	110	3.2	2153	5	CODED FOR BY C. ELEGAN	1.98e-03
17	105	3.1	192	5	COSMID C04E6.	1.39e-02
18	103	3.0	287	4	CD97_HUMAN, PARTIAL CD	2.98e-02
19	101	3.0	483	10	1-CYCLOPROPANE-1-CARBO	6.32e-02
20	98	2.9	165	14	HYPOTHETICAL 17.8 KD P	1.91e-01

21	98	2.9	165	14	069016	HYPOTHETICAL 17.8 KD P	1.91e-01
22	98	2.9	179	14	071195	19.7 KDA PROTEIN.	1.91e-01
23	99	2.9	459	10	082679	ACC SYNTHASE (EC 4.4.1	1.91e-01
24	99	2.9	483	10	096580	1-AMINOCYCLOPROPANE-1-	1.91e-01
25	98	2.9	487	5	093597	F2643.6.	1.91e-01
26	99	2.9	4472	2	033954	TYLACTONE SYNTHASE STA	1.91e-01
27	95	2.8	165	14	070697	HYPOTHETICAL 17.7 KD P	1.91e-01
28	96	2.8	201	2	007640	TRANSCRIPTIONAL REGULA	1.91e-01
29	95	2.8	338	2	045254	HUPU AND HUPV GENES, C	1.91e-01
30	96	2.8	344	2	049638	DCIAP PROTEIN.	1.91e-01
31	94	2.8	482	10	065328	ACC SYNTHASE.	1.91e-01
32	96	2.8	939	5	015799	STRAIN D22 HEAT SHOCK	1.91e-01
33	94	2.8	4331	5	019542	F18C12.1.	1.91e-01
34	92	2.7	165	14	012156	HYPOTHETICAL 17.7 KD P	1.91e-01
35	91	2.7	179	5	020683	F52H3.5.	1.91e-01
36	90	2.7	469	5	077466	THIOASE.	1.91e-01
37	92	2.7	474	10	065210	1-AMINOCYCLOPROPANE-1-	1.91e-01
38	93	2.7	485	10	096579	1-AMINOCYCLOPROPANE-1-	1.91e-01
39	91	2.7	649	5	045067	B0212.1 PROTEIN.	1.91e-01
40	92	2.7	686	4	000187	MASP-2 PROTEIN.	1.91e-01
41	92	2.7	686	4	075754	MASP-2.	1.91e-01
42	91	2.7	939	5	015790	STRAIN 7G8 CG9 (CG9) A	1.91e-01
43	93	2.7	1544	5	013194	SIMILAR TO DROSOPHILA	1.91e-01
44	92	2.7	1732	11	054874	MYOTIC DYSTROPHY KINA	1.91e-01
45	91	2.7	2404	14	090733	POLYPROTEIN.	1.91e-01

ALIGNMENTS

RESULT 1
ID 015328
AC 015328; PRELIMINARY; PRT: 464 AA.

DT 01-JAN-1998 (TREMREL. 05, CREATED)
DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE RET LIGAND 2.
GN RETL2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=LIVER;
RX MEDLINE: 97322356.
RA SANICOLA M., HESSON C.A., MORLEY D.S., CARMILO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PEPINSKI R.B., CAIR R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation
can be mediated by two different cell-surface accessory proteins.";
RL PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
DR EMBL: U97145: G2282028: -
SQ SEQUENCE 464 AA: 51543 MW: 288A8BD8 CRC32:

Query Match 99.9%; Score 3383; DB 4; Length 464;
Best Local Similarity 99.6%; Pred. No. 0.00e+00;
Matches 462; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 MILANVFCLFFFLDITLRLSPSSLOGLGMRPVDCVAVNELCAESNCSSRTTL
|||||
OY 1 MILANVFCLFFFLDITLRLSPSSLOGLGMRPVDCVAVNELCAESNCSSRTTL
|||||
DB 61 ROCLAGDRNTMLANKECOALEVLOESPLYCRRGKRGKKELOCIQIYWSHILN
|||||
OY 61 ROCLAGDRNTMLANKECOALEVLOESPLYCRRGKRGKKELOCIQIYWSHILN
|||||
DB 121 EFYEASPYEPTVSRSLDIFRLASIFSGTGADPVVSAKSHNCLDAKACNLNIN
|||||
OY 121 EFYEASPYEPTVSRSLDIFRLASIFSGTGADPVVSAKSHNCLDAKACNLNIN
|||||
DB 181 YISICRREISPTERCNRKCHALROFPDVPSEYTYRMLFSCODQACVAKH
|||||
OY 181 YISICRREISPTERCNRKCHALROFPDVPSEYTYRMLFSCODQACVAKH
|||||
DB 181 YISICRREISPTERCNRKCHALROFPDVPSEYTYRMLFSCODQACVAKH
|||||
OY 181 YISICRREISPTERCNRKCHALROFPDVPSEYTYRMLFSCODQACVAKH
|||||

Db 241 CSYEDKEKPNCLDLRGVCTDHLCSRLADFHANCRASTQVTSPPADNYQACLSYAGM 300
|||
Oy 241 CSYEDKEKPNCLDLRGVCTDHLCSRLADFHANCRASTQVTSPPADNYQACLSYAGM 300
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Db 301 IGFDMTPNVYDSSPTGIVVSPWCSGSGNMECECEKFLRDTENPCLRNAIQAFGNGTD 360
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Oy 301 IGFDMTPNVYDSSPTGIVVSPWCSGSGNMECECEKFLRDTENPCLRNAIQAFGNGTD 360
|||
Db 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSLSTGTSVITTCSTVOEGGLKANKSKELSM 420
|||
Oy 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSLSTGTSVITTCSTVOEGGLKANKSKELSM 420
|||
Db 421 CFTELTNTIIPGSKNKVIRKPNSGPSRRAPSAALTIVSLMLKIAL 464
|||
Oy 421 CFTELTNTIIPGSKNKVIRKPNSGPSRRAPSAALTIVSLMLKIAL 464
|||
RESULT 2
ID 015316 PRELIMINARY: PRT: 464 AA.
AC 015316:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
GN GDNF-BETA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FETAL BRAIN;
RA WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M.,
RA MOSHINIAKOV M., ATRAKSINEN M.S., PALOTIE A., SARIOLA H., SAARMA M.;
RA SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U93703; G2328737; -
SQ SEQUENCE 464 AA: 51530 MW: DE80D543 CRC32:
Query Match 99.4%; Score 3365; DB 4; Length 464;
Best Local Similarity 99.1%; Pred. No. 0.00e+00;
Matches 460; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
ID 035977 PRELIMINARY: PRT: 464 AA.
AC 035977:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GN GDNF-BETA OR RETL2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC SCUROGNATHI; MORIDAE; MORINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RA TRUPP M., RAYNSCHER C., IBANEZ C.F.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RX MEDLINE: 97322356.
RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PEPINSKY R.B., CATE R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation
can be mediated by two different cell-surface accessory proteins.";
RT PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PEPINSKY R.B., CATE R.L.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF005226; G23232252; -
DR EMBL: U97143; G2282024; -
SQ SEQUENCE 464 AA: 51668 MW: B1A2BD11 CRC32:
Query Match 95.5%; Score 3232; DB 11; Length 464;
Best Local Similarity 94.2%; Pred. No. 0.00e+00;
Matches 437; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

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RESULT 4
ID 035748 PRELIMINARY: PRT: 463 AA.
AC 035748:
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)
DE GDNFR-ALPHA/TRN1-DELTA PROTEIN.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HANNOVER;
RA ZHONG J., ANNIES M., HEUMANN R.;
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ02072; E1154274;
SQ SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;

Query Match 45.3%; Score 1535; DB 11; Length 463;
Best Local Similarity 48.4%; Pred. No. 0.00e+00;
Matches 224; Conservative 101; Mismatches 115; Indels 23; Gaps 19;

Db 2 FLATIFYALPLDILMSAEVSG-GDRLDCKVAKSDQCKECSQSTYRTLRQCVAGKETNF 60
QY 12 FLDDTLRSIASPSSIQGELHGMWRPVDCCVRAHELCAESNCSRYRTLROCLAGRDNN- 70
DB 61 SLTSGLEAKDECRSMELKOKSLYNCRCRKGKKEKNCRLRYSMYOSL-QGNDLLDS 119
QY 71 TM--LANK-ECQALLEVQESPLYDCRCKRGMKELOCLOIYMSIHGLTEGEFEYAS 126
DB 120 PYPENRSLDIFRAVP-F--ISVEHI-S-KGNCLDAKACNLDCTCKYRSAYITPT 174
QY 127 PYPETSLSDIFRLASIFSGTGAIPVSAKSNHCLDAKACNLDNCKLRSSYSTICN 186
DB 175 TSMG-NEVCNRRKCKKALROFPDKVPANHSIGMLFCSCRDIACTERRRQTIIVPCSYER 233
QY 187 REISPTERCNRKCKHAKALROFEDRVSEYTYRMLFCSCQDQACABRRQTIIPSCSYDK 246
DB 234 ERPNCLSLDSCKTNYICRSRLADFTNCOPEBSVSNCLEKNYADCLLAYSGLGTWT 293
QY 247 EKPNCGLDRGVCRTDHLRSRLADHACRASLYOTVTSCPADNYOACISYAGMIGFDMT 306
DB 294 PNYVDS-S-LSVAPMCCSNGNDLEDCLKFLNFKNTCLKNAIOAFNGSDVTMMOP 351
QY 307 PNYVDSPTGIYVSPWCMCGRSGNNEDECEKFLRDTFTENPCLRNAIOAFNGNTVNVSPK 366
DB 352 APPVOTTAATTTAERVANKPLGPAAGSENEIPTHYLPCCANLQAKLSNVSGSTHCLLS 411
QY 367 GPSFCATQAPRY-E-KTSPSLPDLSSTS-LGTSVITTCSTVOEGKLANKSKELSMCFT 423
DB 412 DSDEKDLGAGASSHIITKS-MA-APPSCSLSPVLMITALA 452
QY 424 E-LITNIIIPSGSNKVIKPNSGSRAPSAALTVLSVLMK-LA 463

RESULT 5
ID 035246 PRELIMINARY: PRT: 468 AA.
AC 035246:
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)
DE GDNFR RECEPTOR ALPHA.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL NEUROREPORT 9:0-0(0001).
DR [2]

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RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF014117; G2624961;
SQ SEQUENCE 468 AA; 51751 MW; AFDCE6A1 CRC32;

Query Match 45.1%; Score 1527; DB 11; Length 468;
Best Local Similarity 48.1%; Pred. No. 0.00e+00;
Matches 216; Conservative 104; Mismatches 111; Indels 18; Gaps 15;

Db 16 LMSAEVSG-GDRLDCKVAKSDQCKECSQSTYRTLRQCVAGKETNLSLGLAKDECRS 74
QY 26 LQGPGLHGMWRPVDCCVRAHELCAESNCSRYRTLROCLAGRDNN-TM--LANK-ECQA 80
DB 75 AMELKOKSLYNCRCRKGKKEKNCRLRYSMYOSL-QGNDLLDSYEPVNSRLSDIFR 133
QY 81 ALEVQSPPLYDCRCKRGMKELOCLOIYMSIHGLTEGEFEYASYPEVTSRLSDIFR 140
DB 134 AVPRISVFOOVEHISKGNCLDAKACNLDCTCKYRSAYITPCTSMS-NEVCNRRKC 192
QY 141 LASIFSGTAGDIPVYSAKSNHCLDAKACNLDNCKLRSSYSTICNREISPTERCNRRK 200
DB 193 HKALROFPDKVPANHSYGMLEFCSCRDVACTERRRQTIIVPCSYERERPNCLNDSCKI 253
QY 201 HKALROFPDRVPSEYTYRMLFCSCQDQACABRRQTIIPSCSYEDKEKPNCLDRGVCP 261
DB 261 DILCRSLRDLFANCRASLYOTVTSCPADNYOACISYAGMIGFDMPTNYVDS- 311
QY 311 PMCCSSNGNDLEDCLKFLNFKNTCLKNAIOAFNGSDVTMMOPAPVOTTA 321
DB 321 PMCCSSNGNNECEKFLRDTFTENPCLRNAIOAFNGTIVNVSPKPSFOATQAL 371
QY 371 FRINKPLGPAAGSENEIPTHYLPCCANLQAKLSNVSGSTHCLSDNDYCKGLA 380
DB 380 -KTSPSLPDLSSTS-LGTSVITTCSTVOEGKLANKSKELSMCFT-LITNIIIPSGSN 431
QY 431 HITKS-MA-APPSCSLSPVLMITALA 457
DB 436 VIKPNSGSRAPSAALTVLSVLMK-LA 463

RESULT 6
ID 043912 PRELIMINARY: PRT: 465 AA.
AC 043912:
DT 01-JUN-1998 (TREMBREL. 06, CREATED)
DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
DE GPI-LINKED ANCHOR PROTEIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
SCUROGNATHI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC ANGRIST M., JING S., BOLT S., BENTLEY K., NALLASAMY S., HALUSHKA M.,
RA FOX G.M., CHAKRAVARTI A.;
RL GENOMICS 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;
RA SHEFFELINE S.E., KHORANA S., SCHULTZ P.N., HUANG E., THOBE N., HU 2.J.,
RA FOX G.M., JING S., CORE G.J., GAGEL R.F.;
RL HUM. GENET. 0:0-0(1998).
DR EMBL: AF038420; G2921545; JOINED.
DR EMBL: AF038412; G2921545; JOINED.
DR EMBL: AF038413; G2921545; JOINED.
DR EMBL: AF038414; G2921545; JOINED.
DR EMBL: AF038415; G2921545; JOINED.
DR EMBL: AF038416; G2921545; JOINED.

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1792 GGAACACCATGCTGGCCCAACGAAGAGTGCAGGCGCCCTTGAGAGTCTTGCGAGGAGCC 1851
Db 301 CGCTGACGACTGCGCTGCAAGCGGGCATGAAGAAGAGCTGAGAGTGTGCAGATCT 360
Oy 1852 CGCTGACGACTGCGCTGCAAGCGGGCATGAAGAAGAGCTGAGAGTGTGCAGATCT 1911
Db 361 ACTGAGACATCCACTGGGGCTGACCGAGAGTGTAGAGAGTTCAGAAAGCTTCCCTATG 420
Oy 1912 ACTGAGACATCCACTGGGGCTGACCGAGAGTGTAGAGAGTTCAGAAAGCTTCCCTATG 1971
Db 421 AGCCGTGACCTCCGCTCTGAGACATCTTACGGCTTGTCTTCAATCTTCTAGGAGAG 480
Oy 1972 AGCCGTGACCTCCGCTCTGAGACATCTTACGGCTTGTCTTCAATCTTCTAGGAGAG 2031
Db 481 GGGCAGACCCGCTGCTGACCGCCAGAGACCATTCCTGATCTGTGCAAGGCTCTCA 540
Oy 2032 GGGCAGACCCGCTGCTGACCGCCAGAGACCATTCCTGATCTGTGCAAGGCTCTCA 2091
Db 541 ACCCTGAATGACAATGCAAGAAAGCTGCGCTCTCTACATCTCAATCTGCAACCGCGAGA 600
Oy 2092 ACCCTGAATGACAATGCAAGAAAGCTGCGCTCTCTACATCTCAATCTGCAACCGCGAGA 2151
Db 601 TCTGCGCCACGAGCGCTGCAACCGCCGCAAGTGCACAAAGGCTGCGCCAGTCTTTCG 660
Oy 2152 TCTGCGCCACGAGCGCTGCAACCGCCGCAAGTGCACAAAGGCTGCGCCAGTCTTTCG 2211
Db 661 ACCGGGTGCGCCAGAGTACACCTACCGCATCTCTGCTGCTGCTGCGCAAGACGAGGCT 720
Oy 2212 ACCGGGTGCGCCAGAGTACACCTACCGCATCTCTGCTGCTGCTGCGCAAGACGAGGCT 2271
Db 721 GCGGTGAGCGCGCGCGGCAAAACCATCTGCGCAGCTGCTCTATGAGGACAAAGAGAAAG 780
Oy 2272 GCGGTGAGCGCGCGCGGCAAAACCATCTGCGCAGCTGCTCTATGAGGACAAAGAGAAAG 2331
Db 781 CCAACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Oy 2332 CCAACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2391
Db 841 CCGACTTCATGCAATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Oy 2392 CCGACTTCATGCAATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2451
Db 901 ATTACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Oy 2452 ATTACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2511
Db 961 ATGTGAGCTCCAGGCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Oy 2512 ATGTGAGCTCCAGGCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2571
Db 1021 GGAACATGAGAGAGAGTGTGAGAGTCTCAGGAGCTTCAGCAGAGAACCATGCTCTGC 1080
Oy 2572 GGAACATGAGAGAGAGTGTGAGAGTCTCAGGAGCTTCAGCAGAGAACCATGCTCTGC 2631
Db 1081 GGAACGCAATCCAGGCTTTGGCAAGCGCAGCGAGCTGTAAGCTGTCCCAAAAGGCCCT 1140
Oy 2632 GGAACGCAATCCAGGCTTTGGCAAGCGCAGCGAGCTGTAAGCTGTCCCAAAAGGCCCT 2691
Db 1141 CGTTCCAGGCGCCAGGCGCCCTCGGGGTGAGAGAGCGCTTCTTGGCAGATGACCTCA 1200
Oy 2692 CGTTCCAGGCGCCAGGCGCCCTCGGGGTGAGAGAGCGCTTCTTGGCAGATGACCTCA 2751
Db 1201 GTGACAGTACCAAGCTTGGGAGACAGTGTATACCAACCTGCAAGCTGTGCGAGGAGAG 1260
Oy 2752 GTGACAGTACCAAGCTTGGGAGACAGTGTATACCAACCTGCAAGCTGTGCGAGGAGAG 2811
Db 1261 GGGTGAAGGCCAAACTCCAAAGATTAAAGCATGTGCTTCAAGAGCTCAAGAGCAATA 1320
Oy 2812 GGGTGAAGGCCAAACTCCAAAGATTAAAGCATGTGCTTCAAGAGCTCAAGAGCAATA 2871
Db 1321 TCATCCAGGAGGTAAACAAGTGTAAACCTAACTCAGGCGCCGACGAGAGCCAGACCT 1380

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Oy 2872 TCATCCAGGAGGTAAACAAGTGTAAACCTAACTCAGGCGCCGACGAGAGCTAA... 1380
Db 1381 CGGCTGCTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1441
Oy 2932 CGGCTGCTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1491
Db 1441 CCGAGTCAAGAGATTTTGAAGTACGACAGACAAAGACCGCTGATGAGAAAGAGAG 1501
Oy 2992 CCGAGTCAAGAGATTTTGAAGTACGACAGACAAAGACCGCTGATGAGAAAGAGAG 1551
Db 1501 CACACAGACACACACACACCTTGC 1526
Oy 3052 CACACAGACACACACACACCTTGC 3077

RESULT 3
LOCUS HSU93703 1395 bp mRNA PRI 01-JUN-1999
DEFINITION Human glial cell line-derived neurotrophic factor receptor (GDNF-beta) mRNA, complete cds.
ACCESSION U93703
MID 9228736
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1395)
AUTHORS Martiovaara K., Suanto P., Horelli-Kuitunen N., Lindahl M., Moshnyakov M., Alirakinen M.S., Palotie A., Sariola H. and Suo M.
TITLE Cloning, mRNA distribution and chromosomal localisation of the human glial cell line-derived neurotrophic factor beta, homologue to GDNF-alpha
JOURNAL 2 (bases 1 to 1395)
REFERENCE Suanto P., Martiovaara K. and Saarma M.
TITLE Direct Submision
JOURNAL Submitted (06-MAR-1997) Molecular Neurobiology, Institute of Biotechnology, JP 56, University of Helsinki 00014, Finland
FEATURES
source
1..1395
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/db_xref="taxon:9606"
/chromosome="8"
/map="8p21-p22"
/tissue_type="fetal brain"
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/gene="GDNF-beta"
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/note="forward PCR primer; designed from rat GDNF-beta mRNA"
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/product="glial cell line-derived neurotrophic factor receptor beta"
/db_xref="PID:g3228737"
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BASE COUNT 281 a 463 c 389 g 262 t
ORIGIN
Query Match 32.8%; Score 1387; DB 27; Length 1395;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;

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CEKLRDFTENPCLERNAIOAFNGTDMVMSKPSLSLPTQAPRVEKTPSLPDDISDST
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 ALTALPLMLLAL"

BASE COUNT 647 a 773 c 681 g 686 t

ORIGIN

Query Match 28.8%; Score 1218; DB 29; Length 2787;
 Best Local Similarity 88.7%; Pred. No. 0.00e+00;
 Matches 1425; Conservative 0; Mismatches 177; Indels 5; Gaps 5;

Db 1 CTCGGATTTGGATTTGGGGGCGCTATTCCTGGGCTGTATATATATATGTTATTTTANT 59
 1465 CTCGGATTTGGATTTGGGGGCGCTATTCCTGGGCTGTATATATATATGTTATTTACT 1528
 Db 60 TTTATTTTAAACCTTAAGGAGAAAGACATACACACAAACCTGGGATTTATTTAA 119
 1529 ACTATATATTTTATTTTACCAGAGGAGA-A-AGACAA-AAAAGGTGGGATTTATTTAA 1585
 Db 120 CATGATCTTGGCAAGCCCTTCTGCTCTCTCTTTTATAGCAAAACCTCCGCTCTT 179
 1586 CATGATCTTGGCAAGCCCTTCTGCTCTCTCTTTTATAGCAAAACCTCCGCTCTT 1645
 Db 180 GGCAGACCCCTTCCTCCCTGAGGGCTGTAGCTCCAGCGGCTGGGCGCCCAAGTGAGCTG 239
 1646 GGCAGACCCCTTCCTCCCTGAGGGCTGTAGCTCCAGCGGCTGGGCGCCCAAGTGAGCTG 1705
 Db 240 TGTCCGGGCAATGAGCTGTGTGCGGCTGTAATCAACATGACATCCAGGTACCGACCT 299
 1706 TGTCCGGGCAATGAGCTGTGTGCGGCTGTAATCAACATGACATCCAGGTACCGACCT 1765
 Db 300 TGGGAGTGGCTTGGCAGGCGGGGATTCGAATACATGCTGGGCAATTAAGATGGCAGGC 359
 1766 GGGGAGTGGCTTGGCAGGCGGGGATTCGAATACATGCTGGGCAATTAAGATGGCAGGC 1825
 Db 360 ACCCTTGAAGTCTTTCAGAGAAAGCCCACTGTATGACTCCGCTCAAGCGGGGATGAA 419
 1826 GGCCTTGAAGTCTTTCAGAGAAAGCCCACTGTATGACTCCGCTCAAGCGGGGATGAA 1885
 Db 420 GAAGAGCTGCAAGTGTCTGACAGATCTACTGAGATCCATCTGGGGCTGACAGAGGTGA 479
 1886 GAAGAGCTGCAAGTGTCTGACAGATCTACTGAGATCCATCTGGGGCTGACAGAGGTGA 1945
 Db 480 GGAAGTCTTATGAAGCTTCCCTATGAGCTGTGACCTGGCCCTCTGGAGATCTTACG 539
 1946 GGAAGTCTTATGAAGCTTCCCTATGAGCTGTGACCTGGCCCTCTGGAGATCTTACG 2005
 Db 540 GCTGCTTCAATCTTCTCAGAGAGAGGAGACACCGGGGCTGACATACCAAAAGCAACA 599
 2006 GCTGCTTCAATCTTCTCAGAGAGAGGAGACACCGGGGCTGACATACCAAAAGCAACA 2065
 Db 600 CTGCTGTAGTGGCGGCAAGGCTTGCACCTGATGACATCAAAAGCTTGGCTCTC 659
 2066 CTGCTGTAGTGGCGGCAAGGCTTGCACCTGATGACATCAAAAGCTTGGCTCTC 2125
 Db 660 TTAATCTTCCATCTGCAACCGTGAATCTCTCCACCGAAGCTTCAACCGCGCAAGTG 719
 2126 TTAATCTTCCATCTGCAACCGTGAATCTCTCCACCGAAGCTTCAACCGCGCAAGTG 2185
 Db 720 CCACAGGCTGTGGCGGCAAGTCTTTGACCGGTGGCCAGCGATACCTACCGATGCT 779
 2186 CCACAGGCTGTGGCGGCAAGTCTTTGACCGGTGGCCAGCGATACCTACCGATGCT 2245
 Db 780 CTTTGTCTCTGTCAAGAGCAGCATGTGTAGCGTGGCGGCAAAACCTTCTCCAG 839
 2246 CTTTGTCTCTGTCAAGAGCAGCATGTGTAGCGTGGCGGCAAAACCTTCTCCAG 2305
 Db 840 TTGCTCTTATGAGACAAAGAGAGACCCCACTGCTGGAATGGCCAGCTGTGCTAC 899
 2306 TTGCTCTTATGAGACAAAGAGAGACCCCACTGCTGGAATGGCCAGCTGTGCTAC 2365
 Db 900 AGACCACTGTGGCGGCTCCGACATTTCCAGCGCAACTGTCCAGCTCTCTACCA 959
 2366 TGACCACTGTGGCGGCTCCGACATTTCCAGCGCAACTGTCCAGCTCTCTACCA 2425

Db 960 GACATACACGACGTCTCTCGGAGCAACTACAGGACATGTCTGGCTCTATCTGGCAT 1019
 2426 GACGCTACACGACGTCTCTCGGAGCAACTACAGGACATGTCTGGCTCTATCTGGCAT 2485
 Db 1020 GATTGGGTTTATATGACACCCCAACTATGTGACTCCAAACCCAGGCGCATGTGTGTC 1079
 2486 GATTGGGTTTATATGACACCCCAACTATGTGACTCCAAACCCAGGCGCATGTGTGTC 2545
 Db 1080 TCCCGGTGCAATGTGTGTCGACATGGGAACTGGAAGAGAGTGTGAAGTCTCCAG 1139
 2546 CCCCTGTGTCGCTGTGTGTCGACAGGGAACATGAGAGAGAGTGTGAAGTCTCCAG 2605
 Db 1140 GGAATTCAGGAAACCCATGCTCCGGAATGCAATTCAGGCTTTGATATGACAGAA 1199
 2606 GGAATTCAGGAAACCCATGCTCCGGAATGCAATTCAGGCTTTGATATGACAGAA 2665
 Db 1200 TGTGAACATGTCTCCCAAGGCGCCCTCACTCTCCAGCTAACCCAGGCGCTGGGTGAGAA 1259
 2666 GGTGAACATGTCTCCCAAGGCGCCCTCACTCTCCAGGCTAACCCAGGCGCTGGGTGAGAA 2725
 Db 1260 GACTCTCTCACTGTCAGATGACCTCAAGACAGCAGCAGGCTGGGACAGTGTATCATAC 1319
 2726 GACTCTCTCTCACTGTCAGATGACCTCAAGACAGCAGCAGGCTGGGACAGTGTATCATAC 2785
 Db 1320 CACTGCAATCTATCCAGAGCAAGGCTGTAAGGCCCAACTCCAAAGATTAAAGCAT 1379
 2786 CACTGCAATCTATCCAGAGCAAGGCTGTAAGGCCCAACTCCAAAGATTAAAGCAT 2845
 Db 1380 GTGCTTCAAGAGCTTCAAGCAAAATATCATGCTCCAGGAGTAAAGGTGATCAACTAA 1425
 2846 GTGCTTCAAGAGCTTCAAGCAAAATATCATGCTCCAGGAGTAAAGGTGATCAACTAA 2905
 Db 1440 CTCAGCTCCAGAGCAGCAGCAGTGTGCGCTGCTTCACTGCTCCATCCATCTCATGATGCT 1479
 2906 CTCAGCTCCAGAGCAGCAGCAGTGTGCGCTGCTTCACTGCTCCATCCATCTCATGATGCT 2975
 Db 1500 GACCTTGGCTTGTAGGCTTTGGACCCAG-CACAAAGTCTTTCAGCAACCCAGCA 3025
 2976 GAACTGGCTTGTAGGCTTTGGACCCAG-CACAAAGTCTTTCAGCAACCCAGCA 3075
 Db 1559 TGAATCTCCGCTGACAAATGGAACACACAGCATATACACATGACAC 1605
 3026 TGAATCTCCGCTGACAAATGGAACACACAGCATATACACATGACAC 3072

RESULT 5
 LOCUS AF005226 1395 bp mRNA ROD 02-0111
 DEFINITION Rattus norvegicus glial cell line-derived neurotrophin-1 receptor-beta (GDNFR-beta) mRNA, complete cds.
 ACCESSION AF005226
 MID 92232251
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 REFERENCE 1 (bases 1 to 1395)
 AUTHORS Trupp, M., Raynoschek, C. and Ibanez, C.F.
 TITLE Multiple GPI-anchored receptors control GDNF-dependent independent activation to the c-Ret receptor tyrosine kinase
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1395)
 AUTHORS Trupp, M., Raynoschek, C. and Ibanez, C.F.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAY-1997) Neuroscience, Karolinska Institutet, Doktorsringen 12A, Stockholm 17177, Sweden
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 gene

CDS

/gene="GDNF-beta"
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/function="binds GDNF and allows GDNF binding to and stimulation of the c-ret receptor tyrosine kinase"
/note="GPI-anchored receptor with sequence similarity to GDNF-alpha"
/product="glial cell line-derived neurotrophic factor receptor-beta"
/db_xref="pid:g2232252"
/translation="MILNAFCLFFLDLTLSLSPSSLGSEHGRPPQVDCVRAN ELCAEASNSRRLTLOCLAGDRNTMLANEQALVLESPDYDCRGRKKE LQCLQIWSIHILGDEEFYEAAPYTSRSLDFSLASIFSGDPAVSTKSNH CLDAKACNLNDKRLRSSYSISICNREISPERCRNRKCHALROFEDPASEYTR MLESCODACAERROTILPSCSYEDKRPNCIDRSICRPHDHCRLADPANHCR ASYRTITSCPADNYOACLSYAGMIFDTPNVDNPNPIYIVSPCNCRGSGNMBEE CERFLDFTENPCLRNALIQAFNGIDVNSPKGPSLPATQAPRVEKTPSLPDLDST SLGTSVITTCSTIOEOGLKANSKELSMCTELTNTISPSKVKIKLNGSSRARLSA ALTALPLMLTIAL"

BASE COUNT 309 a 440 c 360 g 286 t

ORIGIN

Query Match 27.18; Score 114.7; DB 29; Length 1395;
Best Local Similarity 91.18; Pred. No. 0.00e+00;
Matches 1271; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Db 1 ATGATCTGGCAAGCGCTCTGCTCTTCTTTTAAAGCAACCTCCGCTCTTG 60
1587 ATGATCTGGCAAGCGCTCTGCTCTTCTTTTAAAGCAACCTCCGCTCTTG 1646
Db 61 GCCAGCCCTTCCTCCGAGGCTGAGCTCCAGCGGCTGGGCCCCCAAGTGAAT 120
1647 GCCAGCCCTTCCTCCGAGGCTGAGCTCCAGCGGCTGGGCCCCCAAGTGAAT 1706
Db 121 GTCGGGGCCAATGAGCTGTGTGGCGTGAATCCAACTGACGTCCAGTACCGACCTT 180
1707 GTCGGGGCCAATGAGCTGTGTGGCGTGAATCCAACTGACGTCCAGTACCGACCTT 1766
Db 181 CGGCACTGCTGCGAGGCGCGGATCCGAATACCATGCTGGCCCAATAGAGTGCAGCA 240
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1827 GCCCTGAGGCTTTGAGAGAGCCCACTATGACTGCGGCTGCAAGCGGGGATGAAG 1886
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1887 AAGGAGCTGCAGTGTGAGATCTACTGAGCATCCACTGGGGCTGACAGAGGTGAG 1946
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2187 CACAAGGCTGCGGCGAGTCTTTGACGCTGTGGCCGAGAGTATACCTACCGATGCTC 2246
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QY 2247 TTCTGCTCTGSCAAGACGAGCGTGCCTGAGCGCCCGGCAACCATCTGCCACG 2306
Db 721 TGCTCTATGAGAGAGAGAGAGAGCCCAACTGCTGAGCTCGGAGCTGTGTGTACA 760
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QY 2367 GACCACTGTGCGCGGTCCCGAGTGGCAGTTCACATGAGCAATGTGAGACCTCTACCG 900
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QY 2967 AAACCTGCGCTGTAG 2981

RESULT 6
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DEFINITION Mus musculus GDNF family receptor alpha 2 (GFRalpha2) mRNA,
complete cds.
ACCESSION AF002701
NID 92145081
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 1392)
Baloh,R.H., Tansey,M.G., Golden,J.P., Crendon,D.J.,
Heuckeroth,R.O., Keck,C.L., Zimonjic,D.B., Popescu,N.C.,
Johnson,E.M. Jr. and Milbrandt,J.
TIR2, a novel receptor that mediates neuritin and GDNF signaling
through Ret
JOURNAL NEURON 18 (5), 793-802 (1997)
MEDLINE 9735791
REFERENCE 2 (bases 1 to 1392)
Baloh,R.H. and Milbrandt,J.D.
AUTHORS Direct Submission

REFERENCE 2 (bases 1 to 1405)
 AUTHORS Wong, Y.W. and Too, H.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-1998) Biochemistry, National University of Singapore, 10, Kent Ridge Crescent, Singapore 119260, Singapore
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BASE COUNT 320 a 430 c 350 g 305 t
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Query Match 19.6% Score 830: DB 29: Length 1405;
 Best Local Similarity 90.1% Pred. No. 3.96e-237;
 Matches 933: Conservative 0: Mismatches 103: Indels 0: Gaps 0:

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 Qy 1941 GGTGAGAGATTACGAGAGCTGCCTATGAGCTGTGACCTCCGCTCTCGAGATC 2000
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 Db 548 TCTCTCACTCATCTGCAACCGGAGATCTCTCCGCAAGAGCTGCAACCGGCGC 607
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RESULT 8
 LOCUS AF079108 1321 bp mRNA ROD 02-DEC-1998
 DEFINITION Mus musculus glial cell line derived neurotrophic factor family receptor alpha 2c (Gfira2) mRNA, complete cds.
 ACCESSION AF079108
 NID g9941705
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrate; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1321)
 AUTHORS Wong, Y.W. and Too, H.P.
 TITLE Identification of mammalian Gfira-2 splice isoforms
 JOURNAL Neuroreport 9 (17) (1998) In press
 REFERENCE 2 (bases 1 to 1321)
 AUTHORS Wong, Y.W. and Too, H.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-1998) Biochemistry, National University of Singapore, 10, Kent Ridge Crescent, Singapore 119260, Singapore.
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 BASE COUNT 306 a 402 c 331 g 282 t
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Query Match 17.9%; Score 758; DB 29; Length 1321;
 Best Local Similarity 89.5%; Pred. No. 7,93e-215;
 Matches 859; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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RESULT 9 GGU90542 2933 bp mRNA VRT 25-JUN-1997
 LOCUS Gallus gallus neuritin receptor alpha (NTNRA1pha) mRNA, complete
 DEFINITION

ACCESSION cds.
 MID 090542
 KEYWORDS 92213804
 SOURCE chicken.

ORGANISM Gallus gallus

Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 2933)

Bui-Bello, A., Adu, J., Plimon, L.G., Horton, A., Thompson, J., Rosenthal, A., Chinchetru, M., Buchman, V.L. and Davies, A.M.

Neuritin response requires a Gpi-linked receptor and

TITLE

Neuritin response requires a Gpi-linked receptor and

JOURNAL

Nature 387 (6634), 721-724 (1997)

MEDLINE

97336104

REFERENCE

2 (bases 1 to 2933)

Buchman, V.L.

AUTHORS

Submitted (24-FEB-1997) Biol. Med. Sciences, Univ. of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS, Scotland

Location/Qualifiers

FEATURES

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CDS

/gene="NTNRA1pha"

polyA_signal

/note="Gpi-linked component of neuritin receptor"

BASE COUNT

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ORIGIN

16.5%; Score 698; DB 21; Length 2933;

Query Match

Best Local Similarity 79.0%; Pred. No. 2.88e-196;

Matches 1011; Conservative 0; Mismatches 259; Indels 9; Gaps 0;

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1583 TACATGATTTTGGCAAGGCTTGTGATGCTCTTTGTAGATGAGACCTCCGCTC 1642

Qy 94 GCTGGCGCCCCCGCTGCCCGCCGAGACCTCCAGGCGCTGGCGGCTGCTGCT 273

1643 TTTGGCAGCCCTTCTCTCTGTCAGGCGCCGAGCTCCAGGCGCTGGCGGCTGCTGCT 273

Db 154 CTGATACGTGCAACAAAGCTGTGTGACGCGAGGAGAGCTGACGCTCCGCTGAC 273

1703 CTGATACGTGCAACAAAGCTGTGTGACGCGAGGAGAGCTGACGCTCCGCTGAC 273

Qy 214 CCGCGGAGAGCTGTGGCGGAGCGAGCGCAACACCATGCTGGCAAGAGAGAG 273

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Db 274 GCGCGCCCTGGAGGTGCTGCAAGAGAGCCGCTGTACAGCTGCTGCAAGAGAG 273

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Qy 334 GAGAAAGGAGATTCAGTGTCTTACGCTTACGATGATACCTCCGCTGCTGCT 273

1883 GAGAAAGGAGATTCAGTGTCTTACGCTTACGATGATACCTCCGCTGCTGCTGCT 273

activation can be mediated by two different cell-surface accessory proteins
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6238-6243 (1997)
 MEDLINE 97323356
 REFERENCE 2 (bases 1 to 3616)
 AUTHORS Santicola, M., Hession, C.A., Worley, D.S., Carmillo, P., Ehrenfels, C., Walsby, L., Robinson, S., Jaworski, G., Wei, H., Tizard, R., Whitley, A., Pepinsky, R.B. and Gale, R.L.
 TITLE Direct Submission
 JOURNAL Submitted (11-APR-1997) Molecular Genetics, BIOGEN, 14 Cambridge Center, Cambridge, MA 02142, USA

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BASE COUNT 876 a 955 c 921 g 864 t
 ORIGIN

Query Match 5.3%: Score 223; DB 29; Length 3616;
 Best local similarity 65.7%: Pred. No. 4,10e-51;
 Matches 592: Conservative 0; Mismatches 297; Indels 12; Gaps 8;

Db 457 GGGCAAGATGATGCCGCTGATGCGCATGAGGCGCTTGAAAGCAAGTCTCTGTACAATG 516
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 Db 517 CCGCTGCAAGCGGGGCGATGAGAAAGAAATGTCTGCGTATCTACTGAGCATGTA 576
 1865 CCGCTGCAAGCGGGGCGATGAGAAAGAAATGTCTGCGTATCTACTGAGCATGTA 1924
 Db 577 CCAGACCTG--C-AGGGAATGACCTCTGGAAGATTCGCCGTATGAGCGGTTAAAG 633
 1925 CCGGCGCTGACCGGAGGAGGAGTTCAGAGGCTCCCTCATGAGCGGTTGACCTC 1984
 Db 634 CAGGTGTCAGATATATTCGCGGAGTCCCGTTCATATCATAGATGTTTCCAGCAATGTA 693
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RESULT 13
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 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murine; Mus.
 REFERENCE 1 (bases 1 to 2549)
 AUTHORS Dey, B.K., Wong, X.W. and Too, H.P.
 TITLE Cloning of a novel murine isoform of the glial cell neurotrophic factor receptor
 JOURNAL Neuroreport 9 (1) (1998) In press
 REFERENCE 2 (bases 1 to 2549)
 AUTHORS Dey, B.K., Wong, X.W. and Too, H.P.
 TITLE Direct Submission
 JOURNAL Submitted (15-JUL-1997) Biochemistry, 10 Kent Ridge Crest Drive, Singapore 119260, Singapore
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 ACCESSION AF042080
 NID 92801556
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominoidea; Homo.
 TITLE
 AUTHORS Sheffield, S.E., Khorana, S., Schultz, P.N., Huang, E., Thobe, N.,
 Hu, Z.J., Fox, G.M., Jing, S., Cole, G.J., and Giegel, R.F.
 JOURNAL Hum. Genet. (1998) In press
 REFERENCE 2 (bases 1 to 1619)
 AUTHORS Sheffield, S.E., Khorana, S., Schultz, P.N., Huang, E., Thobe, N.,
 Hu, Z.J., Fox, G.M., Jing, S., Cole, G.J., and Giegel, R.F.
 TITLE Direct Submission

JOURNAL Submitted (08-JAN-1998) Endocrinology-Box 15, M.D. Anderson Cancer
 Center, 1515 Holcombe Blvd, Houston, TX 77030, USA
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Matches 1488; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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ACCESSION AF005226
KEYWORDS 92232251
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Norway rat.
Rattus norvegicus
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Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1395)
AUTHORS Tripp, M., Raynoschek, C. and Ibanez, C.F.
TITLE Multiple GPI-anchored receptors control GDNF-dependent and
independent activation for the c-ret receptor tyrosine kinase.
JOURNAL Unpublished
2 (bases 1 to 1395)
AUTHORS Tripp, M., Raynoschek, C. and Ibanez, C.F.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1997) Neuroscience, Karolinska Institute
Doktorsringen 12A, Stockholm 17177, Sweden
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FEATURES

Location/Qualifiers

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Qy 1970 TAAAAGGTGATCAAACTTACTAGCTCTCTGAGAGACCGAGAGTGTGACTGCTTGA 2029
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Qy 2030 TGCCCTCCACTCTGTATGTGACTTGCCCT 2061
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RESULT 4

LOCUS HSU97145 2906 bp mRNA PRI 29-JUL-1997

DEFINITION Homo sapiens RET ligand 2 (RETl2) mRNA, complete cds.

ACCESSION U97145

KEYWORDS NID 92282027

SOURCE human.

ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2906)

AUTHORS Sanicola, M., Hession, C.A., Worley, D.S., Carmillo, P., Ehrenfels, C., Walus, L., Robinson, S., Jaworski, G., Wei, H., Tizard, R., Whitley, A., Pepinsky, R.B. and Cate, R.L.

TITLE Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6238-6243 (1997)

MEDLINE 97322356

REFERENCE 2 (bases 1 to 2906)

AUTHORS		Sanicola, M., Hession, C.A., Morley, D.S., Carmillo, P., Ehrenfels, C., Walus, L., Robinson, S., Jaworski, G., Wel, H., Tizard, R., Whitty, A., Pepinsky, R.B. and Cate, R.L.	
TITLE		Direct Submission	
JOURNAL		Submitted (11-APR-1997) Molecular Genetics, BIOGEN, 14 Cambridge Center, Cambridge, MA 02142, USA	
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O	751	AGGCTGTGAGCTCCACGCGTGGCGCCCGCAAGTGGACTGTGTCCGGCCAAATGAGCTGT	810
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D	573	AGATCTACTGAGCATTCACACTGGGGCTGACCGAGGGTGAAGAGTTCACAAAGCTGCC	632
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O	1111	GGACAGGGGACAGCCGGCGGTGACGACCAAAAGCAACACTTGCCTGATGCTGCCAAG	1170
D	753	CCTGAACCTGAATACAACTGCAAGAAGCTGCGCTCTCTCACTCATCTTCATCTGCAC	812
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O	1951	CAATATATCCAGGAGGATTAACAGGTGATCAAACTTACTAGGCCCCCAGCAGAGCA	2010
D	1593	GACCGTGGCTGCTTACCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	1652
O	2011	GACCGTGGCTGCTTACCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	2070
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D	1713	TGGAACACACAGACACACACA 1734	
O	2130	TGGAACACACAGACACACACA 2151	

RESULT 5
 LOCUS AF002700 1526 bp mRNA
 DEFINITION Homo sapiens GNF family receptor alpha 2 (GFRalpha2) mRNA.
 complete cds.
 ACCESSION AF002700
 NID 92145079
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens

|||||
OY 2130 TGGAAACACAGCATACACACA 2151

RESULT 6
LOCUS HSU93703 1395 bp mRNA PRI 01-JUL-1997
DEFINITION Human glial cell line-derived neurotrophic factor receptor beta
(GDNFR-beta) mRNA, complete cds.
ACCESSION U93703
NID 92228736
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 1395)
AUTHORS Martiovaara K., Suvanen P., Horelli-Kuitunen N., Lindahl M.,
Moshayak M., Alakselinen M.S., Palotie A., Sariola H. and Saarma
M.
TITLE Cloning, mRNA distribution and chromosomal localisation of the gene
for the human glial cell line-derived neurotrophic factor beta, a
homologue to GDNFR-alpha
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1395)
AUTHORS Suvanen P., Martiovaara K. and Saarma M.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1997) Molecular Neurobiology, Institute of
Biotechnology, UP 56, University of Helsinki 00014, Finland
FEATURES
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REFERENCE	2 (bases 1 to 1321)
AUTHORS	Wong, Y.M. and Too, H.P.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-1998) Biochemistry, National University of Singapore, 10, Kent Ridge Crescent, Singapore 119260, Singapore
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DEFINITION	Gallus gallus neururin receptor alpha (NTNralpha) mRNA, complete cds.		25-JUN-1997
ACCESSION	U90542		
NID	g2213804		
KEYWORDS			
SOURCE	chicken.		
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REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
AUTHORS	1 (bases 1 to 2933) Bui-Bello,A., Adu,J., Pincin,L.G., Horton,A., Thompson,J., Rosenthal,A., Chinchev,M., Buchman,V.L. and Davies,A.M.		
TITLE	Neururin responsiveness requires a GPI-linked receptor and the Ret receptor tyrosine kinase		
JOURNAL	Nature 387 (6634), 721-724 (1997)		
MEDLINE	97336104		
REFERENCE	2 (bases 1 to 2933) Buchman,V.L.		
AUTHORS	Direct Submission		
TITLE	Submitted (24-FEB-1997) Biol. Med. Sciences, Univ. of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS, Scotland		
JOURNAL			
FEATURES			
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Best Local Similarity 77.7%; Pred. No. 8,32e-195;
Matches 961; Conservative 0; Mismatches 267; Indels 9; Gaps 6;

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RESULT 10
LOCUS AB000800 1415 bp mRNA ROD 04-FEB-1997
DEFINITION Mouse mRNA for GDNF receptor alpha, complete cds.
ACCESSION AB000800
NID 91816441
KEYWORDS GDNF receptor alpha.
SOURCE Mus musculus Dorsal root ganglion Schwann cell cell_line:IMS32
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Scurionath; Muridae;
Murinae; Mus.
1 (bases 1 to 1415)
REFERENCE
AUTHORS Watabe,K.
TITLE Regulation of GDNF receptor alpha mRNA in Schwann cell cultures
JOURNAL Unpublished (1997)
AUTHORS Watabe,K.
TITLE Direct Sublesion
JOURNAL Submitted (30-JAN-1997) to the DDBJ/EMBL/GenBank databases.
Kazuhiko Watabe, Tokyo Metropolitan Institute for Neuroscience,
Neuropathology; Musashidai 2-6, Fuchu, Tokyo 183, Japan
(E-mail:kazut@nms.ac.jp, Tel:0423-25-3881, Fax:0423-21-8678)
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complement(1396..1415)
BASE COUNT 351 a 402 c 358 g 304 t
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Best Local Similarity 65.4%; Pred. No. 4.77e-54;
Matches 584; Conservative 0; Mismatches 297; Indels 12; Gaps
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Oy 890 GGCCAATTAAGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149

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D	796	CAACTGCCACCCAGAGTCAAGGTGTGTGACCAACTGTCTTAAGAGACACTACGAGACTG	855
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RESULT	11
LOCUS	AF014117 2549 bp mRNA ROD 20-NOV-1997
DEFINITION	Mus musculus GDNF receptor alpha (GDNFR-alpha) mRNA, complete cds
ACCESSION	AF014117
NID	g2624960
KEYWORDS	.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryote; Metazoa; Chordata; Vertebrate; Mammalia; Eutheria;
	Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 2549)
AUTHORS	Dey,B.K., Wong,Y.W., and Too,H.P.
TITLE	Cloning of a novel murine isoform of the glial cell line-derived neurotrophic factor receptor
JOURNAL	Neuroreport 9 (1) (1998). In press

REFERENCE	2 (bases 1 to 2549)
AUTHORS	Day,B.K., Wong,Y.W. and Too,H.P.
TITLE	Direct Submission
JOURNAL	Submitted (15-JUL-1997) Blochemistry, 10 Kent Ridge Crescent, Singapore 119260, Singapore
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BASE COUNT	623 a 680 c 693 g 553 t
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Query Match	9.7%; Score 215; DB 29; Length 2545;
Best Local Similarity	65.4%; Pred. No. 4,77e-54;
Matches	584; Conservative 0; Mismatches 297; Indels 12;
Db	1114 GGCCTGATAGTGGCCGACAGCGCTATGAGAGCCTTGAAAGAGAAGTCTCTCTAA...;
QY	890 GGCCTGATAGGAGTGGCCAGCGCCCTGGAGGCTTTCAGGAAAGCCACCTGATAC...;
Db	1174 CCGCTGCAAGGGGGGCATGAAAGAAAGAAATTTGCTGGTATCTACTGGAGCATGTA...;
QY	950 CCGCTGCAAGGGGGGCATGAAAGAAAGAGCTCAGTGTCTGAGATCTACTGGAGCATCA...;
Db	1234 CCAGAGCCTG-CAG--GGAAATGACTACTGGAAGATTCCCATACGAGCCGTTAACAG...;
QY	1010 TCTGGGGGTGACAGAGGTTGAGAGTTCTATGAAAGCTCCCCCATATGAGCCTGTGCTC...;
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QY	1070 GCGGCTCTCGGACATCTTCAGGCTCGGTTCTATCTTCACAGGAGAGGACAGACCTCGG...;
Db	1351 ACACATTTCCAAAGGAAACAAGTGCCTGATGAGCAGCCAGGCTCGACACTGGATGACAC...;
QY	1130 GGTGATCCAAAAGCAACCACTGCTGGATGCGCCCAAGGCTTGCAACTTGAAATGACAA...;
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QY	1190 CTGCAAGAGTGTGGCTCTTATATCTCATCTGCAACCGTAGATCTCTCCACACGA...;
Db	1468 AGTGTGCAACGGCGCAAGTCCACAAAGCCCTCAGGCAAGTCTTTCGACAAAGTTCCAGC...;
QY	1250 ACGGTGCAACGGCGCAAGTCCACAAAGGCTCTGCGCCAGTTCTTTCGACGTTGCCAG...;
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QY	1310 CGAATATACCTACCGCACTGCTTCTGTCTCTGTCAGGACCAAGGAGATGTGTCAGCCGTCG...;
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RESULT	2	PRELIMINARY;	PRT:	464	AA.
ID	015328				
AC	015328:				
DT	01-JAN-1998	(TREMBLREL.	05,	CREATED)	
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DT	01-NOV-1998	(TREMBLREL.	08,	LAST ANNOTATION UPDATE)	
DE	REF. LIGAND 2.				
CN	REF2.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES				
CC	CATARRHINI; HOMINIDAE; HOMO.				

Query Match	93.78;	Score 3131;	DB 4;	Length 464;
Best Local Similarity	94.38;	Pred. No. 0.00e+00;		
Matches 427;	Conservative	17;	Mismatches 9;	Indels 0;
			Gaps	0

OC EUARCTA, METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: PRIMATES:
OC CATARRHINI: HOMINIDAE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FETAL BRAIN.
RA MATIOVARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M.,
RA MASHAYAKOV M., AIRASINEN M.S., PALOTIE A., SARIOLA H., SAARMA M.,
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U95703; G2228757; .
SQ SEQUENCE 464 AA: 51530 MW: DE80D543 CRC32:

Query Match	93.38;	Score 3120;	DB 4;	Length 464;
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Matches 426;	Conservative 17;	Mismatches 10;	Indels 0;	Gaps 0

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Db 72 MLANKECOAALEVLQESPLYOCRCRGMRKELQCIQIWSYHLDLQTEEEFYEASPYEPV 18
Qy 68 MLANKECOAALEVLQESPLYOCRCRGMRKELQCIQIWSYHLDLQTEEEFYEASPYEPV 12
Db 132 TSLRSLDIFRLASIFSGIGADPPVVSAKSNHCLDAAKACNLNDNCKLNSYSISICNREISIP 1
Qy 128 TSLRSLDIFRLASIFSGIGTIDTDAVSTKSNHCLDAKACNLNDNCKLNSYSISICNRLISIP 1
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Qy 188 TERCNRRCCHALROEPFDVPVSEYTYRMLFECSCODQCAERBRROTILPSCSEYENKEXPN 1
Db 252 IDLRGVCRTDHLGCRSLADFHANCRAASYQYTSQPADNYOACLSYAGMIGFDMPINPV 1
Qy 248 IDLRSLCGRTHDLCRSLADFHANCRAASYRTITSCPADNYOACLSYAGMIGFDWTRVAV 1
Db 312 SSPFTIVVSPMNCSCGSGSNMEECEKFLRDTENPCLRNALQAGNGNGDVVNSKGRSTO 1
Qy 308 SSPFTIVVSPMNCSCGSGSNMEECEKFLRDTENPCLRNALQAGNGNGDVVNSKGRSLP 1
Db 372 ATQARVERKTESLPDLDSDSTSLGTSYTTCTSYVOEGSLKANNSKELSMCTELTYTN 1
Qy 368 ATQARVERKTESLPDLDSDSTSLGTSYTTCTSYVOEGSLKANNSKELSMCTELTYTN 1
Db 432 GSNKYIKRNSGSPRRARBPAAALTIVSYVLMKAL 464
Qy 428 GSKYIKRNSGSPRRARLPAAALTIVPLMLLTAL 460

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 WISE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Mar 8 14:31:36 1999; Maspar time 36.56 Seconds
 Tabular output not generated. 694,068 Million cell updates/sec

Title: >US-08-866-354-40
 Description: (1,460) from US08866354.pep
 Perfect Score: 3343
 Sequence: 1 MDVFSHYDETLRLASPS.....RARLSAALPLMLTLAL 460

Scoring table: PAM 150
 Gap 11

Searched: 180763 segs, 55169189 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: strepmb18
 1:sp.Archea 2:sp.Bacteria 3:sp.Fungi 4:sp.Human
 5:sp.Invertebrate 6:sp.Mammal 7:sp.Mhc 8:sp.Organelle
 9:sp.Phage 10:sp.Plant 11:sp.Rodent 12:sp.Unclassified
 13:sp.Vertebrate 14:sp.Virus

Statistics: Mean 47.029; Variance 73.182; scale 0.643
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description	Pred. No.
1	3268	97.8	464	11	GLIAL CELL LINE-DERIVE	0.00e+00
2	3131	93.7	464	4	RET LIGAND 2.	0.00e+00
3	3120	93.3	464	4	GLIAL CELL LINE-DERIVE	0.00e+00
4	1541	46.1	468	11	GDNF RECEPTOR ALPHA.	0.00e+00
5	1539	46.0	463	11	GDNF-ALPHA/TRNRI-DELT	0.00e+00
6	1523	45.6	465	4	GPI-LINKED ANCHOR PROT	0.00e+00
7	1520	45.5	463	11	GDNF RECEPTOR BETA.	0.00e+00
8	1501	44.9	460	4	RET LIGAND 1.	0.00e+00
9	1391	41.6	431	13	GFRA RECEPTOR ALPHA 4 P	0.00e+00
10	777	23.2	397	11	GLIAL CELL LINE-DERIVE	1.02e-164
11	777	23.2	397	11	GLIAL CELL LINE-DERIVE	1.02e-164
12	777	23.2	397	11	GLIAL CELL LINE-DERIVE	1.02e-164
13	708	21.2	400	4	GDNF FAMILY RECEPTOR A	1.13e-16
14	107	3.2	913	5	GDNF FAMILY RECEPTOR A	1.13e-02
15	107	3.2	1016	5	GDNF FAMILY RECEPTOR A	1.13e-02
16	107	3.2	1046	5	GDNF FAMILY RECEPTOR A	1.13e-02
17	107	3.2	1713	11	GDNF FAMILY RECEPTOR A	1.13e-02
18	105	3.1	192	5	GDNF FAMILY RECEPTOR A	1.13e-02
19	103	3.1	287	5	GDNF FAMILY RECEPTOR A	1.13e-02
20	103	3.1	939	5	GDNF FAMILY RECEPTOR A	1.13e-02

Result ID	Score	Match	Length	DB ID	Description	Pred. No.
21	105	3.1	2090	5	GDNF FAMILY RECEPTOR A	1.13e-02
22	105	3.1	2153	5	GDNF FAMILY RECEPTOR A	1.13e-02
23	101	3.0	460	8	GDNF FAMILY RECEPTOR A	1.13e-02
24	99	3.0	1732	11	GDNF FAMILY RECEPTOR A	1.13e-02
25	98	2.9	179	14	GDNF FAMILY RECEPTOR A	1.13e-02
26	96	2.9	201	2	GDNF FAMILY RECEPTOR A	1.13e-02
27	96	2.9	288	5	GDNF FAMILY RECEPTOR A	1.13e-02
28	97	2.9	344	2	GDNF FAMILY RECEPTOR A	1.13e-02
29	96	2.9	368	2	GDNF FAMILY RECEPTOR A	1.13e-02
30	98	2.9	430	2	GDNF FAMILY RECEPTOR A	1.13e-02
31	97	2.9	460	8	GDNF FAMILY RECEPTOR A	1.13e-02
32	98	2.9	478	6	GDNF FAMILY RECEPTOR A	1.13e-02
33	96	2.9	480	11	GDNF FAMILY RECEPTOR A	1.13e-02
34	96	2.9	4131	5	GDNF FAMILY RECEPTOR A	1.13e-02
35	93	2.8	113	14	GDNF FAMILY RECEPTOR A	1.13e-02
36	93	2.8	275	14	GDNF FAMILY RECEPTOR A	1.13e-02
37	93	2.8	302	4	GDNF FAMILY RECEPTOR A	1.13e-02
38	93	2.8	316	3	GDNF FAMILY RECEPTOR A	1.13e-02
39	92	2.8	325	14	GDNF FAMILY RECEPTOR A	1.13e-02
40	94	2.8	650	4	GDNF FAMILY RECEPTOR A	1.13e-02
41	93	2.8	722	4	GDNF FAMILY RECEPTOR A	1.13e-02
42	92	2.8	939	5	GDNF FAMILY RECEPTOR A	1.13e-02
43	93	2.8	1095	11	GDNF FAMILY RECEPTOR A	1.13e-02
44	93	2.8	3857	11	GDNF FAMILY RECEPTOR A	1.13e-02
45	94	2.8	4472	2	GDNF FAMILY RECEPTOR A	1.13e-02

ALIGNMENTS

RESULT 1
 ID 035977; PRELIMINARY: PRT: 464 AA.
 AC 035977;
 DT 01-JAN-1998 (TREMBLER, 05, CREATED)
 DT 01-JAN-1998 (TREMBLER, 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLER, 08, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUTROPHILIC FACTOR RECEPTOR-BETA.
 GN GDNF-ALPHA/TRNRI-DELT.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCINOGNATHI; MURIDAE; MORINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TRUMP M., RAYNOSCHER C., IBANEZ C.F.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RX MEDLINE: 97322356;
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARRILLO P., EHRENFELT S.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins."
 RT PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARRILLO P., EHRENFELT S.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF005226; G2232252;
 DR EMBL: U97143; G2282024;
 SQ SEQUENCE 464 AA: 51668 MW: 61A2BD11 CRC32;
 Query Match 97.8%; Score 3268; DB 11; Length 464;
 Best Local Similarity 99.6%; Pred. No. 0.00e+00;
 Matches 451; Conservative 1; Mismatches 1; Indels 0; Gaps 0

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Merch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Mar 8 14:05:53 1999; Maspar time 16.83 Seconds
 Tabular output not generated. 739.942 Million cell updates/sec

Title: >US-08-866-354-36
 Description: (1.464) from US08866354.pep
 Perfect Score: 3386
 Sequence: 1 MILANVFCLEFFLDLRLS.....RAPSALTVLSVLMKLAL 464

Scoring table:
 PAM 150
 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: swiss-prot36
 1:swissprot

Statistics: Mean 48.016; Variance 67.910; scale 0.707

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3372	99.6	464	1	NRTN_HUMAN	0.00e+00
2	3203	94.6	463	1	NRTN_MOUSE	0.00e+00
3	2686	79.3	465	1	NRTN_CHICK	0.00e+00
4	1534	45.9	468	1	GNDR_MOUSE	0.00e+00
5	1527	45.1	468	1	GNDR_HUMAN	0.00e+00
6	1521	44.9	464	1	GNDR_CHICK	0.00e+00
7	1501	44.3	469	1	GNDR_MOUSE	0.00e+00
8	100	3.0	462	1	EFNU_HUMAN	3.18e-02
9	103	3.0	1712	1	TGFB_RAT	9.87e-03
10	97	2.9	354	1	NOV_MOUSE	9.98e-02
11	95	2.8	113	1	RL19_MYCTU	2.10e-01
12	95	2.8	408	1	B3AR_HUMAN	2.10e-01
13	91	2.7	342	1	CYS2_HAECO	8.96e-01
14	91	2.7	342	1	CYS1_HAECO	8.96e-01
15	91	2.7	352	1	ASBP2_BLAG	8.96e-01
16	91	2.7	427	1	MODS_YEAST	8.96e-01
17	91	2.7	438	1	NO55_HUMAN	8.96e-01
18	93	2.7	452	1	EFNU_BOVIN	4.37e-01
19	90	2.7	513	1	HDAC_MAIZE	1.28e+00
20	91	2.7	521	1	GAG_SIVAG	8.96e-01
21	93	2.7	799	1	TRKA_RAT	4.37e-01
22	91	2.7	879	1	LDR_RAT	8.96e-01
23	92	2.7	1603	1	PSC_DROME	6.27e-01

ID	Query Match	Score	Length	ID	Description	Pred. No.
24	92	2.7	2410	1	POLL_BAYM	GENOME POLYPEPTIDE 1 (
25	92	2.7	2412	1	POLL_BAYM	GENOME POLYPEPTIDE 1 (
26	88	2.6	113	1	RL19_MYCTU	505 RIBOSOMAL PROTEIN
27	89	2.6	302	1	UT49_VZVD	TEGMENT PROTEIN (GENE
28	89	2.6	354	1	FUT2_RABIT	GALACTOSIDE 2-L-FUCOSY
29	88	2.6	379	1	GAL7_HUMAN	ESTRADIOL 17 BETA-DEHY
30	88	2.6	381	1	DBH2_MOUSE	BETA-3 ADRENERGIC RECE
31	88	2.6	418	1	B3AR_MACW	MAIZE DEHYDROGENASE (
32	88	2.6	432	1	MDHC_MAIZE	MAIZE DEHYDROGENASE (
33	88	2.6	463	1	TIS_SALPO	TYPE I RESTRICTION ENZ
34	88	2.6	480	1	HD11_XENLA	PROBABLE HISTONE DEACE
35	88	2.6	621	1	ASPA_AERSA	MICROBIAL SERINE PROTE
36	89	2.6	646	1	PLAP_MOUSE	PHOSPHOLIPASE A-2-ACTI
37	89	2.6	796	1	TRKA_HUMAN	HIGH AFFINITY NERVE GR
38	89	2.6	808	1	VGB_HSVSA	GLYCOPROTEIN B PRECUR
39	88	2.6	854	1	LDR_RTRIG	LOW-DENSITY LIPOPROTEI
40	88	2.6	863	1	SIP1_YEAST	SIP1 PROTEIN.
41	88	2.6	873	1	PC1_HUMAN	PLASMA-CELL MEMBRANE
42	87	2.6	1115	1	PAN2_YEAST	PAB-DEPENDENT POLY(A)-
43	89	2.6	1408	1	SERR_DROME	SERRATE PROTEIN PRECU
44	89	2.6	2703	1	NORC_DROME	NEUROGENIC LOCUS NORC
45	88	2.6	2871	1	FBN1_BOVIN	FIBRILLIN 1 PRECURSOR

ALIGNMENTS

RESULT	ID	Query Match	Score	Length	ID	Description	Pred. No.
1	NRTN_HUMAN	99.6%	3372	464	1	NRTN_HUMAN	0.00e+00
2	NRTN_MOUSE	94.6%	3203	463	1	NRTN_MOUSE	0.00e+00
3	NRTN_CHICK	79.3%	2686	465	1	NRTN_CHICK	0.00e+00
4	GNDR_MOUSE	45.9%	1534	468	1	GNDR_MOUSE	0.00e+00
5	GNDR_HUMAN	45.1%	1527	468	1	GNDR_HUMAN	0.00e+00
6	GNDR_CHICK	44.9%	1521	464	1	GNDR_CHICK	0.00e+00
7	GNDR_MOUSE	44.3%	1501	469	1	GNDR_MOUSE	0.00e+00
8	EFNU_HUMAN	3.0%	100	462	1	EFNU_HUMAN	3.18e-02
9	TGFB_RAT	3.0%	103	1712	1	TGFB_RAT	9.87e-03
10	NOV_MOUSE	2.9%	97	354	1	NOV_MOUSE	9.98e-02
11	RL19_MYCTU	2.8%	95	113	1	RL19_MYCTU	2.10e-01
12	B3AR_HUMAN	2.8%	95	408	1	B3AR_HUMAN	2.10e-01
13	CYS2_HAECO	2.7%	91	342	1	CYS2_HAECO	8.96e-01
14	CYS1_HAECO	2.7%	91	342	1	CYS1_HAECO	8.96e-01
15	ASBP2_BLAG	2.7%	91	352	1	ASBP2_BLAG	8.96e-01
16	MODS_YEAST	2.7%	91	427	1	MODS_YEAST	8.96e-01
17	NO55_HUMAN	2.7%	91	438	1	NO55_HUMAN	8.96e-01
18	EFNU_BOVIN	2.7%	93	452	1	EFNU_BOVIN	4.37e-01
19	HDAC_MAIZE	2.7%	90	513	1	HDAC_MAIZE	1.28e+00
20	GAG_SIVAG	2.7%	91	521	1	GAG_SIVAG	8.96e-01
21	TRKA_RAT	2.7%	93	799	1	TRKA_RAT	4.37e-01
22	LDR_RAT	2.7%	91	879	1	LDR_RAT	8.96e-01
23	PSC_DROME	2.7%	92	1603	1	PSC_DROME	6.27e-01

Matches 461: Conservative 2: Mismatches 1: Indels 0: Gaps 0:

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Db 1 MILANVCLFFELDETLRLSLASSPSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Oy 1 MILANVCLFFELDETLRLSLASSPSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Db 61 RCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Oy 61 RCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Db 121 EYEASPEPYTSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKCNLNDCKKLSS 180
Oy 121 EYEASPEPYTSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKCNLNDCKKLSS 180
Db 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCODQACAEERRQTIIPS 240
Oy 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCODQACAEERRQTIIPS 240
Db 241 CSYEDKEKPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSQPADNYQACLSYAGM 300
Oy 241 CSYEDKEKPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSQPADNYQACLSYAGM 300
Db 301 IGFDMPYVYDSSPTGIYVSPWCSCRGSGNMECEKEFLDFTENPCRLNAIQAFNGTD 360
Oy 301 IGFDMPYVYDSSPTGIYVSPWCSCRGSGNMECEKEFLDFTENPCRLNAIQAFNGTD 360
Db 361 VVNSPKGPTFSQATQAPREKTPSLPDDLSSTLSGTSTVITCTSTVOEGKANKSKELSM 420
Oy 361 VVNSPKGPTFSQATQAPREKTPSLPDDLSSTLSGTSTVITCTSTVOEGKANKSKELSM 420
Db 421 CFTELTTNIIPGSKVKIKPNSGSRAPSAITVLSVLMKCAL 464
Oy 421 CFTELTTNIIPGSKVKIKPNSGSRAPSAITVLSVLMKCAL 464

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RESULT 2 STANDARD: PRT: 463 AA.

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AC 008842:
ID NRTR_MOUSE
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
DE (GDNF-BETA).
GN GFRA2 OR GDNFRB OR TRNR2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HEICKENROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
RA JOHNSON E.M., JR., HILBRANDT J.;
RA NEURON 18:793-802(1997).
RL -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
CC AND IN THE ADRENAL.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
DR EMBL: AF002701; G2145082; -.
DR MGI: MGI:1195462; GFRA2.
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 443 TGF-BETA RELATED NEUROTROPHIC FACTOR

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FT PROPEP 444 463 RECEPTOR 2.
FT CARBOHYD 52 52 HYDROPHOBIC, REMOVED DURING MATURATION.
FT CARBOHYD 357 357 (POTENTIAL).
FT CARBOHYD 413 413 (POTENTIAL).
FT LIPID 443 413 POTENTIAL.
FT VARSPLIC 14 146 GPI-ANCHOR (POTENTIAL).
SO SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32; MISSING (IN SHORT FORM).

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Query Match 94.6%; Score 3203; DB 1; Length 463;
Best Local Similarity 93.5%; Pred. No. 0.00e+00;
Matches 433; Conservative 19; Mismatches 11; Indels 0; Gaps

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Db 1 MILANVCLFFELDETLRLSLASSPSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Oy 1 MILANVCLFFELDETLRLSLASSPSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Db 61 RCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Oy 61 RCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Db 121 EYEASPEPYTSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKCNLNDCKKLSS 180
Oy 121 EYEASPEPYTSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKCNLNDCKKLSS 180
Db 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCODQACAEERRQTIIPS 240
Oy 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCODQACAEERRQTIIPS 240
Db 241 CSYEDKEKPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSQPADNYQACLSYAGM 300
Oy 241 CSYEDKEKPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSQPADNYQACLSYAGM 300
Db 301 IGFDMPYVYDSSPTGIYVSPWCSCRGSGNMECEKEFLDFTENPCRLNAIQAFNGTD 360
Oy 301 IGFDMPYVYDSSPTGIYVSPWCSCRGSGNMECEKEFLDFTENPCRLNAIQAFNGTD 360
Db 361 VVNSPKGPTFSQATQAPREKTPSLPDDLSSTLSGTSTVITCTSTVOEGKANKSKELSM 420
Oy 361 VVNSPKGPTFSQATQAPREKTPSLPDDLSSTLSGTSTVITCTSTVOEGKANKSKELSM 420
Db 421 CFTELTTNIIPGSKVKIKPNSGSRAPSAITVLSVLMKCAL 463
Oy 421 CFTELTTNIIPGSKVKIKPNSGSRAPSAITVLSVLMKCAL 463

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RESULT 3 STANDARD: PRT: 465 AA.

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AC 013157:
ID NRTR_CHICK
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (GDNF
DE RECEPTOR BETA) (GDNF-BETA).
GN GFRA2 OR GDNFRB.
OS GALUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE:
RA BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
RA ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
RA NATURE 387:721-724(1997)
RL -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
DR EMBL: U90542; G221805; -.
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.

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FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 445 NEUTURIN RECEPTOR ALPHA.
 FT PROPEP 446 465 HYDROPHOBIC, REMOVED DURING MATURATION
 FT CARBOHYD 355 355 (POTENTIAL).
 FT CARBOHYD 387 387 POTENTIAL.
 FT CARBOHYD 412 412 POTENTIAL.
 FT LIPID 445 445 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 465 AA: 51908 MM: SCA073E4 CRC32;

Query Match 79.3% Score 2686; DB 1; Length 465;
 Best Local Similarity 74.7% Pred. No. 0.00e+00;
 Matches 349; Conservative 70; Mismatches 43; Indels 5; Gaps 3;

Db 1 MILANAFIVVDETLTSLAAPSPGODLOGMVRPDCIANKLCAEGSCSSRYTL 60
 QY 1 MILANFCLFFLDLTLSLSPSSLOPELHGRPPDYDCVANKLCAESNCSSRYTL 60
 Db 61 RQCLAGDRNTMLANKECQALLEVLOESPLYDCRCRGMREIOCLQYWSIHGLAGE 120
 QY 61 RQCLAGDRNTMLANKECQALLEVLOESPLYDCRCRGMREIOCLQYWSIHGLAGE 120
 Db 121 EFYEASPEYPTSRSLDIFRLASTISG--DPATSKSNHCLDAKACNLNCKRLSG 178
 QY 121 EFYEASPEYPTSRSLDIFRLASTISG--DPATSKSNHCLDAKACNLNCKRLSG 180
 Db 179 YISTCSKEISATEHCSSRRKCHALROFPDNPSEYTYRLFCSCDKQACAPRROTIVF 238
 QY 181 YISICNREISPTERCNRKCHALROFPDNPSEYTYRLFCSCDKQACAPRROTIVF 240
 Db 239 CSYEDKERNCLDLRNVCRADHLCSRSLADFHANCOASFOSLSCPGDNYOACLSYTL 298
 QY 241 CSYEDKERNCLDLRNVCRADHLCSRSLADFHANCOASFOSLSCPGDNYOACLSYTL 300
 Db 299 IGFDTPRYVAVASTSITISPCSCSGCNLEEECEKRLPOTEPCLRNAIQAGNSTD 358
 QY 301 IGFDTPRYVAVASTSITISPCSCSGCNLEEECEKRLPOTEPCLRNAIQAGNSTD 360
 Db 359 VNLSPKNSPTITMLPKVEKSPALPDINDSNVMTDTSITTCSTIOEHGOKLNKSKOS 418
 QY 361 VNLSPKNSPTITMLPKVEKSPALPDINDSNVMTDTSITTCSTIOEHGOKLNKSKOS 419
 Db 419 LCYSETQITDTPDQKTFVDOKAAGSRHARILPAVPIVLKLL 465
 QY 420 MCFTE--LTNIIIPGSKNVIKPNSGSRAPSAALTIVSLMKLAL 464

RESULT 4
 ID GDNF_RAT STANDARD; PRT: 468 AA.
 AC 062997;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (GDF-BETA RELATED
 NEUROTROPIC FACTOR RECEPTOR 1) (RET LIGAND 1).
 GN GFRAL OR GDNFRA OR TRNRI OR RETL.
 OS RATTUS NORVEGICUS (RAT).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINA.
 RX MEDLINE: 96270513.
 RA JING S., WEN D., YU Y., HOLST P.L., LIO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTROCK B.W.,
 RA FOX G.M.;
 RL CELL 85:1113-1124(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MISTAR; TISSUE-KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,

RA PEPINSKY R.B., CATE R.L.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96273032.
 RA TREANOR J.J.S., GOODMAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,
 RA BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI F.,
 RA PHILLIPS H.S., GODDARD A., MOORE M.W., BUI-BELLU A., DAVIES A.M.,
 RA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;
 RL NATURE 382:80-83(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 DR EMBL: U59486; G139863;
 DR EMBL: U97142; G282022;
 KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 430
 FT PROPEP 431 468
 FT DOMAIN 362 369
 FT CARBOHYD 59 59
 FT CARBOHYD 347 347
 FT CARBOHYD 406 406
 FT LIPID 430 430
 SQ SEQUENCE 468 AA: 51649 MM: 6A7A2B2A CRC32;
 Query Match 45.9% Score 1554; DB 1; Length 468;
 Best Local Similarity 48.2% Pred. No. 0.00e+00;
 Matches 223; Conservative 102; Mismatches 120; Indels 18; Gaps 1;

Db 2 FLATLYALPELIDILMSAEVSG--GDRLDVYKASDOCLCEQSCSTRYTLRQCVAKETNF 11
 QY 12 FLDTLTLSLSPSSLOPELHGRPPDYDCVANKLCAESNCSSRYTLRQCLAGDRN- 70
 Db 61 SLTGLAKDECRAMALOKSLYNGCRCKRGMKKNCLRTIYSMSQSL--QGNITLFIN 11
 QY 71 TM--LANK--ECQALLEVLOESPLYDCRCRGMREIOCLQYWSIHGLTECHRYV 11
 Db 120 PVEPNRSLDIFRAVPEISDFQOVHISNGNCLDAKACNLNCKRLSG 11
 QY 127 PVEPYTSLDIFRLASTISGTDGADPVYSAKSNHCLDAKACNLNCKRLSG 11
 Db 180 TSMS-NEVCNRRKCHALROFPDNPSEYTYRLFCSCDKQACAPRROTIVF 11
 QY 187 REISPTERCNRKCHALROFPDNPSEYTYRLFCSCDKQACAPRROTIVF 11
 Db 239 ERPNCLSLDSCKNTYCRSLADFTNCPDESNSVNCLEKNYADCLLAYSGILTYV 11
 QY 247 EKPNCCLDRGCRDHLCSRSLADFHANCRASAYOTVSCPADNYOACLSYAGMICH 11
 Db 299 PNVDSS--S--LSVAPWCDGSGNDLEDCLKEFLFNDNCTKNAIOAFNGSPVTM 11
 QY 307 PNVDSSPTGIVVSPWCSGSGSGNMECEKFLFNDNCTKNAIOAFNGSVNVPK 11
 Db 357 APPVOTTTATTTAFRVRNKPPLGAGSENEIPTVLPCCANLQAKLSNVSGSTI 11
 QY 367 GPSQAOAPRV-E-KTPSLPDDSDTS--LGTSVITTCISVOGGLKANKSKRLN 11
 Db 417 DSDGKGLAGASSHITTKS-MA-APPSCLSLSPVIMLTALA 457
 QY 424 E--LTNIIIPGSKNVIKPNSGSRAPSAALTIVSLMKL-LA 463

RESULT 5
 ID GDNF_MOUSE STANDARD; PRT: 468 AA.
 AC P97785;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

	D	DT	15-JUL-1998 (REL.	.36,	LAST ANNOTATION UPDATE).
	DE	GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED.			
	DE	NEUROTROPHIC FACTOR RECEPTOR 1).			
	GN	GFRAL OR GDNRA OR TRNR1.			
	OS	MUS MUSCULI (MOUSE).			
	OC	EUDAROTA; METAZOA;			
	CC	EUTHERIA; RODENTIA.			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	GC	TISSUE-DORSAL ROOT GANGLION:			
	RA	NATASE K.;			
	RL	SUBMITTED (FEB-1997)			
	CC	-1-	FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY SIMILARITY).		
	CC	-1-	SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET (BY SIMILARITY).		
	CC	-1-	SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).		
	CC	-1-	SIMILARITY: BELONGS TO THE GDNFR FAMILY.		
	DR	EMBL: AB000800; GI816442; -.			
	KM	MGI:1100842; GFRAL.			
	RV	RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.			
	FT	CHAIN	1	24	POTENTIAL.
	FT	SIGNAL	25	430	GDNF RECEPTOR ALPHA.
	FT	PROPEP	431	468	HIDROPHOBIC, REMOVED DURING MATURATION (POTENTIAL). THR-RICH. POTENTIAL. POTENTIAL. POTENTIAL. GPI-ANCHOR (POTENTIAL).
	FT	DOMAIN	362	369	CARBONYD 59 59 CARBOHYD 347 347 CARBOHYD 406 406 FT LIPID 430 430 SEQUENCE 468 AA: 51782 KM: 6C6dClB2 CRC32;
	SO				

Query Match	45.1%;	Score 1527;	DB 1;	Length 468;
Best Local Similarity	48.1%;	Pred. No. 0.00e+00;		
Matches	216;	Conservative	104;	Mismatches 111;
			Indels	18;
			Gaps	15

ID	GDNR_HUMAN	STANDARD:	PRT:	464 AA.
AD	P56159;			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED			
DE	NEUROPHILIC FACTOR RECEPTOR 1).			
GN	GFRA1 OR GDNFRA OR TRNR1.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUMETAZOA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-SUBSTANTIA NIGRA;			
RX	MEDLINE; 96270513.			
RA	JING S., WEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMIR R.,			
RA	ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,			
RA	FOX G.M.;			
RL	CELL. 85:1113-1124(1996).			
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED			
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY			
CC	SIMILARITY).			
CC	-1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX			
CC	WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY			
CC	SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY			
CC	SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.			
DR	MM; 601496; -.			
KW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.			
FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	428	GDNF RECEPTOR ALPHA.
FT	PROPEP	429	464	HYDROPHOBIC. REMOVED DURING MATURATION
FT				(POTENTIAL).

Query Match	44.98;	Score 1521;	DB 1;	Length 464;
Best Local Similarity	48.38;	Pred. No. 0.00e+00;		
Matches	223;	Conservative	100;	Mismatches 121;
				Indels 18;
				Gaps 0;

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Db      2 FLATLYEALPPLDILLLSAEVSG-GRDLDCYKASDOCLKEOSGSKTYRTLRCQVACCKTIRNP :  
        || :::: |::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| :::  
Qy     12 FLDDTLRSLASPSSIQGPFLHGWRRPPVDCAVRANELCAAESNCSRSRYTLKICQLLNQNNRP :
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Db      61 SLASGLEAKDECRAMEALQKSLYNCRRCRGMKKKENCLRIYWSMYSQI--CGM--
      :: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     71 TM---LANK-ECQAALLEVLDQSPLYDCRCRGMKKRELQCLQIYWSIHGLTICHHM--

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Db 120 PYPVPNSRLSDIFRVPVPEISDVFOOVEHIPKGNCCLDAAKACNLDDICKKIKYKAYTGTG
      ||||| ||||| : ||| : ||||| ||||| : ||| ||||| :
QY 127 PYPVPVTSRLSDIFRLASIFSTGTGADPVVSAKSNHCDAAKACNLNDNCKKLRKSYTSTG

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Db 180 TSVS-NDVCNRRKCHKALQFEDKVPAAKHSYGMLEFSCSRDIACETERROTIVPVOSTHAA...
      :: : ||| ||| ||| ||| : : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Qy 187 REISPTERCNRRKCHKALQFEDKVPSEIYTYRMLFSCQDQACAERRQTIILPSCSYENK...

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Db      239  EKPNCL-IQDSCKTNYICRSRLADEFTNCPESRSVSSCKENYADCLLAYSLGIVMI
          ||||| : |:|: ||||| : |||: ||| : |||: ||| : |||: ||| : |||: |||
QY      247  EKPNCLDRGVGCRDHLCSRRLADEHANCRASTYQITSCPADNYQACLSGYAGMTGFTY

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D6      298 PNYIDSS-S-LSVAPMCDSCNSGNDLEBCLKFLNFKDNTCLKNAIDAFNGSDV VVV :  
        |||::: : |||| | || | || | : |||:|||||::: |  
QY      307 PNVDSSPTGIIVSPMCRCRSGGNMBEECEFLRDPTENPCLRNAIDAFNGNJNVNV SIK :
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Db      356 APPVQTTATTATTAALRVKKKPLGPGAGSENEPLTHVLPPCANLQAOAKKSNVSGNTIHLCS "
      367 GPSFOATAPRV-E-KTPSLPDDLS DSTS-LGTSVITTCSTQEOGLKANKSNELSMCFI "
QY

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DB	416	NGNRECEGLASSHITTS-NA-APPSGSLPLVLT-AL	454
OY <td>424</td> <td>ELTNIIP-GSNKVIKRNPSGRAPRAPSALVLSYMLKAL</td> <td>464</td>	424	ELTNIIP-GSNKVIKRNPSGRAPRAPSALVLSYMLKAL	464
RESULT	7	STANDARD:	PRT: 469 AA.
ID	GNDR	CHICK	
AC	01356:		
DT	01-NOV-1997	(REL. 35, CREATED)	
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)	
DE	GNDR RECEPTOR ALPHA PRECURSOR (GNDR-ALPHA)	(TGF-BETA RELATED	
DE	NEUROTHORPHIC FACTOR RECEPTOR 1).		
GN	GNDRAL OR GNDRFA.		
OS	GALLUS GALLUS (CHICKEN).		
OC	EDUAROTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPLATA: AVES: NEOGNATHAE;		
OC	GALLIFORMES.		
OC	REPTILIFORMES.		
OC	SEQUENCE FROM N.A.		
RC	TISSUE-BRAIN:		
RA	BUU-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,		
RA	ROSENTHAL A., CHICHESTER M., BUCHMAN V.L., DAVIES A.M.;		
RL	NATURE 387:721-724(1997).		
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED		
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY		
CC	STIMULARITY).		
CC	-1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX		
CC	WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET		
CC	(BY STIMULARITY).		
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY		
CC	STIMULARITY).		
CC	-1- STIMULARITY: BELONGS TO THE GDNFR FAMILY.		
DR	EMBL: U90541; G2213803;		
KW	RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.		
FT	SIGNAL	1	27
FT	CHAIN	28	430
FT	PROPEP	431	469
FT	DOMAIN	361	368
FT	CARBOHYD	62	62
FT	CARBOHYD	163	163
FT	CARBOHYD	346	346
FT	CARBOHYD	405	405
FT	LIPID	430	430
SO	SEQUENCE	469 AA; 52043 MW; C8D241C9 CRC32;	
Query Match	44.38;	Score 1501;	DB 1; Length 469;
Best Local Similarity	50.78;	Pred. No. 0.00e+00;	
Matches	224;	Conservative	92; Mismatches 101; Indels 25; Gaps 18;
Db	30	LDCVNASDOCKEIOESCSTKRYRTLRCVAGKSNFSRATGLERAKDECKSAMALOKSLYN	89
OY	38	VDCVRANLCLCAESKSSRYRTLQCLAGR-----RNTMLANK-ECQAALEVLQESLDY	92
Db	90	CRCKRGKMKKCNLCRIIYMSYQSL-QGNDLLEDSPEYEVNSRLSDIFRLAIVS--VEP	145
OY	93	CRCKRGKMKKELQCLQIYMSIHGLGTEGEEFEYASPEYEVNTRSLSDIFRLASIFSGTADP	152
Db	146	VLS-KGNNCIDAAACNNDTCRKFRAIYIPCCSSNS-NCICKRKRCHRALRFFDKVP	203
OY	153	VVSASNSNICIDAAACNNDCKKLRSYISICRREISPFERCKRRCHRALRQFFDRVP	212
Db	204	PKHSGMFCSCRDVACTERRRORTIVPVCSEYDERKPCNLIQESCKKNYICRSRLADF	263
OY	213	SEYTRMLFCCQOQOQOQERRRORTILPSCSEYDERKPCDLDREVCRDHLCRSLADF	272
Db	264	TNCPDEBSVSSCKENYADCLLAYSGLIGVTMPNTYIDS-S-LSYAPWCDCSNGSNDI	321
OY	273	ANCRASYOTIVTSCPADNYOACLGSAAGMIGCDMPNYVDSPTIIVSPWCSCGSGNME	332
Db	322	DECRELNFPODNTCLKNAIOAFNGGVDYVNWOPILPQVTTATT--TASLTKNTGSETT	380
OY	333	EECEKEFLDFTENPCPLRNAIOAFNGGIVNWNVSPKGPSQAQADARVEKTPSLPDLSDDST	392

DB	381	NNEIPTHNDSPACANLQAKKRKNSVDEIETCLNENAIKNDTPGVTSHISENSEFAL	440
OY	333	S--LGT-SVITTCISVDEOGL-KANNSEKLSMCTE--LTTNIIPG-SNKVIRP-NS-G-442	
Db	441	PTSEFYPSTPLILMTI-ALSLFL	461
OY	443	PSRAPSPALVLSVLMKIAL	464
RESULT	8	STANDARD;	452 AA.
ID	EFU_HUMAN	PTI;	452 AA.
AC	P49411		
DT	01-FEB-1996 (REL. 33, CREATED)		
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)		
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)		
DE	ELONGATION FACTOR TU, MITOCHONDRIAL PRECURSOR (P43).		
GN	TUFM.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-LIVER;		
RC	MEDLINE; 96138557.		
RA	MORIAN V.L., BURKHART W.A., SPREMUILLI L.L.;		
RL	BIOCHIM. BIOPHYS. ACTA 1264:347-356(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-KIDNEY, AND HEART;		
RX	MEDLINE; 97473528.		
RA	LING M., MERANTE F., CHEN H.-S., DUFE C., DUNCAN A.M.V.,		
RA	ROBINSON B.H.;		
RL	GENE 197:325-336(1997).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-LIVER;		
RX	MEDLINE; 95129693.		
RA	WELLS J., HENKLER F., LEVERSHA M., KOSHY R.;		
RL	FEBS LETT. 358:119-125(1995).		
RN	[4]		
RP	PARTIAL SEQUENCE OF 44-54.		
RC	TISSUE-HEART;		
RA	DUNN M.J.;		
RL	SUBMITTED (MAR-1996) TO THE SWISS-PROT DATA BANK.		
CC	-1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF		
CC	AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN		
CC	BIOSYNTHESIS.		
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL.		
CC	EMBL; L388995; G704416; -.		
DR	EMBL; X84694; G899285; -.		
DR	EMBL; S75463; G833999; ALT_INIT.		
DR	HSC-ZDPAGE; P49411; HUMAN.		
DR	MIM; 602389; -.		
DR	PROSITE; PS00301; EFACOR_GTP: 1.		
KW	ELONGATION FACTOR; PROTEIN BIOSYNTHESIS; MITOCHONDRION;		
KW	TRANSIT PEPTIDE; GTP-BINDING.		
FT	TRANSIT	1	43
FT	CHAIN	44	452
FT	NP_BIND	64	71
FT	NP_BIND	126	130
FT	NP_BIND	181	184
FT	CONFLICT	195	197
FT	CONFLICT	384	384
SO	SEQUENCE	452 AA;	49541 MW; F29C75C3 CRC32;

DB 291 ELLGSKNRTVTGT 306
OY 169 NLNDCKKLRSYSYIS 184

RESULT 9
ID TGF β -RAT STANDARD: PRT: 1712 AA.

AC 000918;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR
DE (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-
GN 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT).
OS RATUS NORVEGICUS (RAT).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; MAMMALIA.
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA TSUJI T., OKADA F., YAMAGUCHI K., NAKAMURA T.;
RX MEDLINE: 91062373.
CC PROC. NATL. ACAD. SCI. U.S.A. 87:8835-8839(1990).
CC -1- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS
CC COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH
CC A MASKING PROTEIN CONSISTING OF A DISULFIDE-BONDED COMPLEX OF A
CC DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETA1 PRECURSOR AND
CC A THIRD COMPONENT DENOTED TGF-BETA1-BP (OR MP LARGE SUBUNIT).
CC TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.
CC -1- SIMILARITY: CONTAINS 18 EGF-LIKE DOMAINS.
DR EMBL: M55431; G207286;
DR HSSP: P19398; LATA.
DR PROSITE: PS00010; ASX_HYDROXYL. 13.
DR PROSITE: PS00022; EGF_1; 2.
DR PROSITE: PS01186; EGF_2; 10.
DR PROSITE: PS01187; EGF_CA; 15.
KW GROWTH FACTOR BINDING; REPEAT: EGF-LIKE DOMAIN; HYDROXYLATION; SIGNAL.
FT SIGNAL 1 20
FT PROPEP 21 736
FT CHAIN 737 1577
FT SITE 734 736
FT SITE 1575 1577
FT PROPEP 1578 1712
FT DOMAIN 181 213
FT DOMAIN 391 423
FT DOMAIN 531 604
FT REPEAT 618 658
FT DOMAIN 671 721
FT REPEAT 721 906
FT DOMAIN 907 948
FT DOMAIN 949 989
FT DOMAIN 990 1029
FT DOMAIN 1030 1070
FT DOMAIN 1071 1111
FT DOMAIN 1112 1152
FT DOMAIN 1153 1193
FT DOMAIN 1194 1235
FT DOMAIN 1236 1277
FT DOMAIN 1278 1320
FT REPEAT 1340 1392
FT REPEAT 1415 1457
FT DOMAIN 1458 1498
FT REPEAT 1517 1568
FT DOMAIN 1612 1652
FT DOMAIN 1653 1697
FT DISULFID 185 195
FT DISULFID 189 201
FT DISULFID 203 212
FT DISULFID 395 405
FT DISULFID 399 411

FT DISULFID 413 422
FT DISULFID 622 633
FT DISULFID 628 642
FT DISULFID 644 657
FT DISULFID 659 672
FT DISULFID 676 689
FT DISULFID 692 705
FT DISULFID 706 719
FT DISULFID 720 733
FT DISULFID 734 747
FT DISULFID 748 761
FT DISULFID 762 775
FT DISULFID 776 789
FT DISULFID 790 803
FT DISULFID 804 817
FT DISULFID 818 831
FT DISULFID 832 845
FT DISULFID 846 859
FT DISULFID 860 873
FT DISULFID 874 887
FT DISULFID 888 901
FT DISULFID 902 915
FT DISULFID 916 929
FT DISULFID 930 943
FT DISULFID 944 957
FT DISULFID 958 971
FT DISULFID 972 985
FT DISULFID 986 999
FT DISULFID 1000 1013
FT DISULFID 1014 1027
FT DISULFID 1028 1041
FT DISULFID 1042 1055
FT DISULFID 1056 1069
FT DISULFID 1070 1083
FT DISULFID 1084 1097
FT DISULFID 1098 1111
FT DISULFID 1112 1125
FT DISULFID 1126 1139
FT DISULFID 1140 1153
FT DISULFID 1154 1167
FT DISULFID 1168 1181
FT DISULFID 1182 1195
FT DISULFID 1196 1209
FT DISULFID 1210 1223
FT DISULFID 1224 1237
FT DISULFID 1238 1251
FT DISULFID 1252 1265
FT DISULFID 1266 1279
FT DISULFID 1280 1293
FT DISULFID 1294 1307
FT DISULFID 1308 1321
FT DISULFID 1322 1335
FT DISULFID 1336 1349
FT DISULFID 1350 1363
FT DISULFID 1364 1377
FT DISULFID 1378 1391
FT DISULFID 1392 1405
FT DISULFID 1406 1419
FT DISULFID 1420 1433
FT DISULFID 1434 1447
FT DISULFID 1448 1461
FT DISULFID 1462 1475
FT DISULFID 1476 1489
FT DISULFID 1490 1503
FT DISULFID 1504 1517
FT DISULFID 1518 1531
FT DISULFID 1532 1545
FT DISULFID 1546 1559
FT DISULFID 1560 1573
FT DISULFID 1574 1587
FT DISULFID 1588 1601
FT DISULFID 1602 1615
FT DISULFID 1616 1629
FT DISULFID 1630 1643
FT DISULFID 1644 1657
FT DISULFID 1658 1671
FT DISULFID 1672 1685
FT DISULFID 1686 1699
FT DISULFID 1700 1713
FT CARBOHYD 370 370
FT CARBOHYD 416 416
FT CARBOHYD 612 612
FT CARBOHYD 1042 1042
FT CARBOHYD 1242 1242
FT CARBOHYD 1357 1357

SO SEQUENCE 1712 AA; 186598 MW; 7C924D81 CRC32;

Query Match 3.0%; Score 103; DB 1; Length 1712;
Best Local Similarity 34.9%; Pred. No. 9, 87e-03;
Matches 15; Conservative 12; Mismatches 12; Indels 4; Gaps 4;

DB 1032 DECLOP-RVCT-NGSCTNLESGYMSCKGVSPT-P-DHRHCQ 1070
OY 159 NHCLDAKACNLNDCKKLRSYSYISICNREISPTERCNRRKH 201

RESULT 10
ID NOV MOUSE STANDARD: PRT: 354 AA.
AC 064299;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
 GN NOV.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV, AND ICR: TISSUE-BRAIN;
 RA SNAITH M.R., NATARAJAN D., TAYLOR L.B., CHOI C.P., MARTINERIE C.,
 RA PERBAL B., SCHOFIELD P.N., BOULTER C.A.;
 RN SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 96204003.
 RA MARTINERIE C., CHEVALIER G., RAUSCHER F.J. III, PERBAL B.;
 RL ONCOGENE 12:1479-1492(1996).
 CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
 CC GROWTH REGULATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY. CEF-10/CYR61/CTCFG/EISP-12/NOV PROTEIN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).
 DR EMBL: X97863; E181580; -;
 DR EMBL: Y09257; E281106; -;
 DR EMBL: X96585; E28599; -;
 DR MGD: MGI:109185; NOV
 DR PROSITE: PS00222; IGF_BINDING; 1.
 DR PROSITE: PS01185; CTCK_1; 1.
 DR PROSITE: PS01225; CTCK_2; 1.
 DR PROSITE: PS01208; VWFC; 1.
 KM PROTO-ONCOGENE: GROWTH FACTOR BINDING: SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 354 NOV PROTEIN HOMOLOG.
 FT DOMAIN 102 168 VWFC.
 FT DISULFID 261 335 CTCK.
 FT DISULFID 261 298 BY SIMILARITY.
 FT DISULFID 278 312 BY SIMILARITY.
 FT DISULFID 289 328 BY SIMILARITY.
 FT DISULFID 292 330 BY SIMILARITY.
 FT DISULFID 297 334 BY SIMILARITY.
 FT CARBOHYD 91 91 POTENTIAL.
 FT CARBOHYD 277 277 POTENTIAL.
 SQ SEQUENCE 354 AA: 38928 MW: 65446 F0E CRC32:
 Query Match 2.9%; Score 97; DB 1; Length 354;
 Best Local Similarity 36.2%; Pred. No. 9.98e-02;
 Matches 17; Conservative 10; Mismatches 17; Indels 3; Caps 3;
 Db 260 KCLRTKSLKAIHLOFENCSTLYTKRFGVCSGDSRCCTPHNKT1 306
 Oy 194 RCNR-RKCHKALROFEPVSEYTYRMLFCS-COD-OACAEERRRQTI 237
 RESULT 11
 ID RL19.MYCTU STANDARD; PRT: 113 AA.
 AC Q10792;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L19.
 GN RPLS OR MTCY274.35C.
 OS MYCOBACTERIUM TUBERCULOSIS.
 OC PROKARYOTA; FIRMITUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SUBUNIT
 CC INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION OF THE
 CC AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS.

DR EMBL: Z74024; E248891; -;
 DR PROSITE: PS01015; RIBOSOMAL_L19; 1.
 KM RIBOSOMAL PROTEIN.
 SQ SEQUENCE 113 AA: 13013 MW: 913A74FE CRC32:
 Query Match 2.8%; Score 95; DB 1; Length 113;
 Best Local Similarity 46.2%; Pred. No. 2.10e-01;
 Matches 12; Conservative 4; Mismatches 10; Indels 0; Caps 0;
 Db 5 DEVDKPSLDDIPAEVPCDTIVHYK 30
 Oy 341 DEFDNPLRNALIAQAFGNGTVNVSPK 366
 RESULT 12
 ID B3AR-HUMAN STANDARD; PRT: 408 AA.
 AC P13945;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE BETA-3 ADRENERGIC RECEPTOR.
 GN ADRB3 OR ADRB3R OR B3AR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89368947.
 RA EMORINE L.J., MARULLO S., BRIEND-SUTREN M.-M., PATEY G., TATE K.,
 RA DELAVIER-KLUTCHKO C., STROSBERG A.D.;
 RL SCIENCE 245:1118-1121(1989).
 RN [2]
 RP REVISIONS, SEQUENCE FROM N.A.
 RX MEDLINE: 93279311.
 RA VAN SPRONSEN A., NAHMIA S., KRIEF S., BRIEND-SUTREN M.-M.,
 RA STROSBERG A.D., EMORINE L.J.;
 RL EUR. J. BIOCHEM. 213:1117-1124(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93285320.
 RA LELIAS J.M., KAGHAD M., RODRIGUEZ M., CHALON P., BONNIN J.,
 RA DUPRE I., DELPECH B., BENSARD M., LEFUR G., FERRARA P., CAPUT D.,
 RL FEBS LETT. 324:127-130(1993).
 RN [4]
 RP SEQUENCE OF 392-408 FROM N.A.
 RX MEDLINE: 93125503.
 RA GRANNEMAN J.G., LAHNERS K.N., RAO D.D.;
 RL MOL. PHARMACOL. 42:964-970(1992).
 RN [5]
 RP VARIANT ARG-64.
 RA CLEMENT K., VAISSE C., MANNING B.S.J., BASDEVANT A., GUY-GRANDI N.,
 RA RUIZ J., SILVER K.D., SHULDINER A.R., FROGUEL P., STROSBERG A.L.;
 RL NEW ENGL. J. MED. 333:352-354(1995).
 RN [6]
 RP VARIANT ARG-64.
 RX MEDLINE: 96361936.
 RA FUJISAWA T., IREGAMI H., YAMATO E., TAKEKAWA K., NAKAGAWA Y.,
 RA HAMADA Y., OGA T., UEDA H., SHINTANI M., FUKUDA M., OGIHARA I.;
 RL DIABETOLOGIA 39:349-352(1996).
 RN [7]
 RP VARIANT ARG-64.
 RX MEDLINE: 96217306.
 RA CANDELORE M.R., DENG L., TOTA L.M., KELLY L.J., CASCIERI M.A.,
 RA STRADER C.D.;
 RL ENDOCRINOLOGY 137:2638-2641(1996).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G-
 CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AN
 CC THERMOGENESIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: MAINLY IN ADIPOSE TISSUES.
 CC -1- POLYMORPHISM: THE VARIANT ARG-64 SEEMS TO BE ASSOCIATED WITH
 CC WEIGHT GAIN (OBESITY) AND TO IS ALSO ASSOCIATED WITH

CC SUSCEPTIBILITY TO NON-INSULIN-DEPENDENT DIABETES MELLITUS (NIDDM).
 CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: M29932: G178896; ALT_TERM.
 DR EMBL: X70812: E67465; ALT_SEQ.
 DR EMBL: X72861: G298095; -
 DR EMBL: X70811: G312397; -
 DR EMBL: X70812: E281052; ALT_SEQ.
 DR EMBL: X70812: E280975; ALT_SEQ.
 DR EMBL: S53291: G263089; -
 DR PIR: A41348: A41348.
 DR PIR: S33751: S33751.
 DR GCRDB: GCR_0051; -
 DR GCRDB: GCR_0547; -
 DR GCRDB: GCR_0595; -
 DR GCRDB: GCR_0735; -
 DR MIM: 109691; -
 DR PROSITE: PS00237: G-PROTEIN_RECEPTOR_1.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KM MULTIGENE FAMILY; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE;
 KM POLYMORPHISM; DIABETES; OBESITY.
 FT DOMAIN 1 36
 FT TRANSMEM 37 62
 FT DOMAIN 64 72
 FT TRANSMEM 73 91
 FT DOMAIN 92 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT TRANSMEM 156 178
 FT DOMAIN 179 203
 FT TRANSMEM 204 225
 FT DOMAIN 226 292
 FT TRANSMEM 293 314
 FT DOMAIN 315 326
 FT TRANSMEM 327 347
 FT DOMAIN 348 408
 FT CARBOHYD 8 8
 FT CARBOHYD 26 26
 FT CARBOHYD 110 189
 FT DISULFID 361 361
 FT LIPID 64 64
 FT VARIANT 64 64
 FT SEQUENCE 408 AA; 43519 MW; 47AEC098 CRC32;
 Query Match 2.88; Score 95; DB 1; Length 408;
 Best Local Similarity 39.4%; Pred. No. 2.10e-01;
 Matches 13; Conservative 10; Mismatches 8; Indels 2; Gaps 2;
 Db 296 LMGFTLCMLPEFLANVRAIGSPVGPAPF 328
 Oy 1 MILAN-VFC-LFFFLDDTLRLSPSLGPEL 31
 RESULT 13
 ID CYS1_HAECO STANDARD: PRT: 342 AA.
 AC P25733:
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE CATHEPSIN B-LIKE CYSTEINE PROTEINASE 2 PRECURSOR (EC 3.4.22.-).
 GN AC-2.
 OS HAEMONCHUS CONTORTUS.
 OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; SPIRURIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91218800.
 RA PRATT D., COX G.N., MILHAUSEN M.J., BOISVENUE R.J.:
 RL MOL. BIOCHEM. PARASITOL. 43:181-192(1990).
 CC -1 FUNCTION: EXPRESSION OF THE PROTEASE CORRELATES WITH BLOOD-FEEDING
 CC AND SUGGESTS A ROLE FOR THE PROTEASE IN BLOOD DIGESTION.
 CC -1 DEVELOPMENTAL STAGE: AT LOW LEVEL IN THE THIRD AND FOURTH-STAGE
 CC LARVAE, AND ABUNDANT IN ADULT WORMS.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAININ FAMILY OF THIOL PROTEASES.
 CC -1 SIMILARITY: STRONGEST, TO CATHEPSIN B.

DR EMBL: M60213: G159165; -
 DR EMBL: M60212: G159165; JOINED.
 DR PIR: A44965; A44965.
 DR HSSP: P07858; IHUC.
 DR PROSITE: PS00139: THIOL_PROTEASE_CYS_1.
 DR PROSITE: PS00639: THIOL_PROTEASE_HIS_1.
 DR PROSITE: PS00640: THIOL_PROTEASE_ASN_1.
 KM HYDROLASE; THIOL PROTEASE; ZYMOGEN; GLYCOPROTEIN; SIGNAL;
 FT SIGNAL 1 7
 FT PROPEP 86 86
 FT CHAIN 87 342
 FT ACT_SITE 114 114
 FT ACT_SITE 114 114
 FT ACT_SITE 285 285
 FT ACT_SITE 305 305
 FT DISULFID 100 128
 FT DISULFID 111 156
 FT DISULFID 147 214
 FT DISULFID 148 152
 FT DISULFID 185 218
 FT DISULFID 193 205
 FT CARBOHYD 99 99
 FT CARBOHYD 138 138
 FT CARBOHYD 198 198
 FT SEQUENCE 342 AA; 38406 MW; 89092341 CRC32;
 Query Match 2.7%; Score 91; DB 1; Length 342;
 Best Local Similarity 33.3%; Pred. No. 8.96e-01;
 Matches 12; Conservative 9; Mismatches 12; Indels 3; Gaps 3;
 Db 200 TYEGEC-RGTAPTPPC-RRKCRPGVKKRY-RIDKRY 232
 Oy 180 SYISICNREISPTERCNRKCHKALROFEDRVPSRY 215
 RESULT 14
 ID CYS1_HAECO STANDARD: PRT: 342 AA.
 AC P19092:
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE CATHEPSIN B-LIKE CYSTEINE PROTEINASE 1 PRECURSOR (EC 3.4.22.-).
 GN AC-1.
 OS HAEMONCHUS CONTORTUS.
 OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; SPIRURIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-ISOLATE BELL;
 RX MEDLINE: 90348715.
 RA COX G.N., PRATT D., HAGEMAN R., BOISVENUE R.J.:
 RL MOL. BIOCHEM. PARASITOL. 41:25-34(1990).
 CC -1 FUNCTION: EXPRESSION OF THE PROTEASE CORRELATES WITH BLOOD-FEEDING
 CC AND SUGGESTS A ROLE FOR THE PROTEASE IN BLOOD DIGESTION.
 CC -1 DEVELOPMENTAL STAGE: AT LOW LEVEL IN THE THIRD AND FOURTH-STAGE
 CC LARVAE, AND ABUNDANT IN ADULT WORMS.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAININ FAMILY OF THIOL PROTEASES.
 CC -1 SIMILARITY: STRONGEST, TO CATHEPSIN B.
 DR EMBL: M31112: G159173; -
 DR PIR: A45524; A45524.
 DR HSSP: P07858; IHUC.
 DR PROSITE: PS00139: THIOL_PROTEASE_CYS_1.
 DR PROSITE: PS00639: THIOL_PROTEASE_HIS_1.
 DR PROSITE: PS00640: THIOL_PROTEASE_ASN_1.
 KM HYDROLASE; THIOL PROTEASE; ZYMOGEN; GLYCOPROTEIN; SIGNAL;
 FT SIGNAL 1 7
 FT PROPEP 86 86
 FT CHAIN 87 342
 FT ACT_SITE 114 114
 FT ACT_SITE 285 285
 FT ACT_SITE 305 305

FT DISULFID 100 128 BY SIMILARITY.
 FT DISULFID 111 156 BY SIMILARITY.
 FT DISULFID 147 214 BY SIMILARITY.
 FT DISULFID 148 152 BY SIMILARITY.
 FT DISULFID 185 218 BY SIMILARITY.
 FT DISULFID 193 205 BY SIMILARITY.
 FT DISULFID 99 99 POTENTIAL.
 FT CARBOHYD 138 138 POTENTIAL.
 FT CARBOHYD 198 198 POTENTIAL.
 FT CARBOHYD 296 296 POTENTIAL.
 SQ SEQUENCE 342 AA; 38459 MW; 290E7705 CRC32;

Query Match 2.7%; Score 91; DB 1; Length 342;
 Best Local Similarity 33.3%; Pred. No. 8,96e-01;
 Matches 12; Conservative 9; Mismatches 12; Indels 3; Gaps 3;

Db 200 TYGEC-RGTAPTPC-KKCRPGVKKMY-RIDKRY 232
 QY 180 SYISICNREISPTERCNRKCKKALROFDRPSEY 215

RESULT 15
 ID ASP2_BLAG STANDARD; PRT: 352 AA.
 AC P54958;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ASPARTIC PROTEASE BLA G 2 PRECURSOR (EC 3.4.23.-) (ALLERGEN BLA G II).
 OS BLATTELLA GERMANICA (GERMAN COCKROACH).
 OC EDKARYOTA; METAZOA; ARTHROPODA; INSECTA; BLATTODEA.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE: 95370299.
 RA ARRUDA L.K., VALLES L.D., MANN B.J., SHANNON J., FOX J.W.,
 RA VEDVICK T.S., HAYDEN W.L., CHAPMAN M.D.;
 RL J. BIOL. CHEM. 270:19563-19568(1995).
 CC -1- FUNCTION: MAJOR ALLERGEN; FUNCTIONS AS A DIGESTIVE ENZYME IN THE
 CC COCKROACH.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE
 CC EUKARYOTIC ASPARTYL PROTEASES FAMILY.
 DR EMBL: U28863; G1176397; -
 DR PROSITE: PS00141; ASP_PROTEASE; FALSE_NEG.
 KW HYDROLASE; ASPARTYL PROTEASE; SIGNAL; ALLERGEN; ZYMOGEN.
 FT SIGNAL 1 7
 FT PROPEP ? 24
 FT CHAIN 25 352 ASPARTIC PROTEASE BLA G 2.
 FT ACT_SITE 35 35 BY SIMILARITY.
 FT ACT_SITE 239 239 BY SIMILARITY.
 FT CARBOHYD 117 117 POTENTIAL.
 FT CARBOHYD 295 295 POTENTIAL.
 FT CARBOHYD 340 340 POTENTIAL.
 SQ SEQUENCE 352 AA; 38558 MW; 23F3B608 CRC32;

Query Match 2.7%; Score 91; DB 1; Length 352;
 Best Local Similarity 32.3%; Pred. No. 8,96e-01;
 Matches 20; Conservative 16; Mismatches 20; Indels 6; Gaps 6;

Db 34 FINTOYAGITKIGNONF-LT-VFDSISCN-VYVA-SQECVGACVCPNL-OKYEKPKY 88
 QY 123 YEASPYEPVTSRLSDIFRLASIFSGTGADPYVASKSNHCLDAKAC-NLNDNCKKLRSSY 181
 Db 89 IS 90
 QY 182 IS 183

Search completed: Mon Mar 8 14:06:44 1999
 Job time : 51 secs.

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(TM)

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MSPcrh_pp    protein - protein database search, using Smith-Waterman algorithm
Run on:      Mon Mar 8 14:53:57 1999;  MasPar time 17.15 Seconds
              779.553 Million cell updates/sec
Tabular output not generated.

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Title: >US-08-866-354-43
Description: (1-498) from US08866354 pep
Perfect Score: 2337
Sequence: 1 MXXLXXXXPPXXMXMXLX.....XLPVMTALAXLLSXXXX 498
```

Scoring table: PAM 150
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 08

Listing first 45 summaries

Database: swiss-prot36
1:swlsprot

Statistics: Mean 45.078; Variance 68.218; scale 0.661

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1803	77.2	468	1	GDNR_RAT	GDNR RECEPTOR ALPHA PR	0.00e+00
2	1788	76.5	454	1	NRRR_HUMAN	NEUTRININ RECEPTOR ALP	0.00e+00
3	1772	76.0	453	1	NRRR_MOUSE	NEUTRININ RECEPTOR ALP	0.00e+00
4	1772	75.8	468	1	GDNR_MOUSE	GDNR RECEPTOR ALPHA PR	0.00e+00
5	1758	75.2	464	1	GDNR_HUMAN	GDNR RECEPTOR ALPHA PR	0.00e+00
6	1599	68.4	469	1	GDNR_CHICK	GDNR RECEPTOR ALPHA PR	0.00e+00
7	1561	66.8	465	1	NRRR_CHICK	NEUTRININ RECEPTOR ALP	0.00e+00
8	108	4.6	2524	1	NOTC_XENLA	NEUROGENIC LOCUS NOTCH	6.55e-04
9	105	4.5	2871	1	FBN1_HUMAN	FIBRILLIN 1 PRECURSOR	2.15e-03
10	104	4.5	2871	1	FBN1_HUMAN	FIBRILLIN 1 PRECURSOR	3.18e-03
11	102	4.4	381	1	DHB2_MOUSE	ESTRADIOL 17 BETA-DEHY	6.92e-03
12	102	4.4	2871	1	FBN1_BOVIN	FIBRILLIN 1 PRECURSOR	6.92e-03
13	97	4.2	1964	1	NT4_MOUSE	NEUROGENIC LOCUS NOTCH	4.59e-02
14	97	4.2	3051	1	YNA3_CAEEL	HYPOTHETICAL PROTEIN T	4.59e-02
15	95	4.1	427	1	YBAC_ECOLI	HYPOTHETICAL 46.1 KD P	9.60e-02
16	95	4.1	816	1	NEL_MOUSE	NEL PROTEIN PRECURSOR	9.60e-02
17	93	4.0	488	1	YSMS_CAEEL	HYPOTHETICAL 56.3 KD P	1.98e-01
18	93	4.0	816	1	NEL_RAT	NEL PROTEIN PRECURSOR	1.98e-01
19	94	4.0	879	1	LIDR_RAT	LOW-DENSITY LIPOPROTEI	1.38e-01
20	93	4.0	1460	1	SLIT_HUMAN	SLIT PROTEIN PRECURSOR	1.98e-01
21	93	4.0	2444	1	NTG1_DROME	NEUROGENIC LOCUS NOTCH	1.98e-01
22	90	3.9	382	1	ALBU_HUMAN	SERUM ALBUMIN (FRAEMEN	5.76e-01
23	92	3.9	383	1	DLK_HUMAN	DELTA-LIKE PROTEIN PRE	2.84e-01

24	91	3.9	396	1	EPIA_GIALA	ELONGATION FACTOR 1-AL	4.05e-01
25	90	3.9	565	1	HENA_SYSCM	HEMAGGLUTININ-NEURAMIN	5.76e-01
26	90	3.9	757	1	COMP_HUMAN	CARTILAGE OLIGOMERIC M	5.76e-01
27	91	3.9	826	1	MSL_MOUSE	CELL SURFACE ANTIGEN M	4.05e-01
28	92	3.9	880	1	D1.DROME	NEUROGENIC LOCUS DELTA	2.84e-01
29	90	3.9	2531	1	NTG1_RAT	NEUROGENIC LOCUS NOTCH	5.76e-01
30	92	3.9	2911	1	FBN2_HUMAN	FIBRILLIN 2 PRECURSOR.	8.16e-01
31	89	3.8	249	1	ULN3_HCWA	PROTEIN UL103.	8.16e-01
32	88	3.8	384	1	GAS1_MOUSE	GROWTH-ARREST-SPECIFIC	1.13e+00
33	88	3.8	385	1	DLK_MOUSE	DELTA-LIKE PROTEIN PRE	1.13e+00
34	89	3.8	509	1	AVPL_RAT	ACTIVIN RECEPTOR TYPE	8.16e-01
35	89	3.8	603	1	FAI2_CAVPO	COAGULATION FACTOR XII	8.16e-01
36	89	3.8	854	1	LDRR_CRICK	LOW-DENSITY LIPOPROTEI	8.16e-01
37	89	3.8	1013	1	CHS2_EMEMI	CHITIN SYNTHASE 2 (EC	8.16e-01
38	88	3.8	1217	1	EGF_MOUSE	EPIDERMAL GROWTH FACTO	1.15e+00
39	89	3.8	1700	1	BAB3_CHITE	BALBINI RING PROTEIN	8.16e-01
40	89	3.8	1712	1	TGBB_RAT	LATENT TRANSFORMING GR	8.16e-01
41	88	3.8	2351	1	NTG1_MOUSE	NEUROGENIC LOCUS NOTCH	1.15e+00
42	87	3.7	755	1	COMP_RAT	CARTILAGE OLIGOMERIC M	1.62e+00
43	87	3.7	816	1	NEL_HUMAN	NEL PROTEIN PRECURSOR	1.62e+00
44	87	3.7	1808	1	TEVA_CHICK	TENASCIN PRECURSOR (TN	1.62e+00
45	87	3.7	2703	1	NORC_DROME	NEUROGENIC LOCUS NOTCH	1.62e+00

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	468 AA.
ID	GDNF_RAT			
AC	062997;			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	GDNF RECEPTOR ALPHA PRECURSOR (GNFR-ALPHA) (TGF-BETA RELATED			
DE	NEUROTROPHIC FACTOR RECEPTOR 1) (RET LGAND 1).			
CN	GERAL OR GNFRFA OR TRNR1 OR RETLL.			
OS	KARTOVA NORVEGICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
NC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=RETINA.			
RX	MEDLINE: 96670513.			
RA	JING S., WEN D., YU Y., HOLST P.L., LIO Y., FANG M., TAMIR R.,			
RA	ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHOCK B.W.,			
RA	FOX G.M.;			
RL	CELL. 85:1113-1124(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MISTAR; TISSUE=KIDNEY;			
RX	MEDLINE: 97322356.			
RA	SANICOLO M., HESSON C.A., MONLEY D.S., CARMILO P., EHRENFELS C.,			
RA	WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITY A.,			
RA	PEPINSKY R.B., CAKE R.T.;			
RA	PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 96673032.			
RA	TREADOR J.V.S., GOOGMAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,			
RA	BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HETTI F.,			
RA	PHILLIPS H.S., GODDARD A., MOORE M.W., BU-BELLO A., DAVIS A.M.,			
RA	ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.V.,			
RL	NATURE 382:80-83(1996).			
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED			
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.			
CC	-1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX			
CC	WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.			
CC	-1- SIMILARITY: BELONGS TO THE GDNF FAMILY.			
CC	EMBL: U59486; GI399863; -			
CC	EMBL: U97142; G2282022; -			
FW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.			
WT	SIGNAL	1	24	POTENTIAL.

FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT 362 369 (POTENTIAL).
 FT DOMAIN 59 59 POLY-THR.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT CARBOHYD 430 430 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 468 AA; 51649 MW; 6A7A2B2A CRC32;

Query Match 77.2%; Score 1803; DB 1; Length 468;
 Best Local Similarity 53.3%; Pred. No. 0.00e+00;
 Matches 255; Conservative 23; Mismatches 183; Indels 17; Gaps 12;

1 MFATLAFALPLDLMLSAEVSQDRL--DCVVASDQCKEKGSCSTRTLRQCVAGRET 58
 16 MKLXLSTLPLXLLQGLGELXRLXDXCVAXXXCAEXXCSXXYTLRQCAAGXX 75
 59 NFSLTSLGELAKDE--CRSAMEALKOKSLYNCRCRGMKREKNCRLRYMSYSLQ--GNDL 115
 76 NFXLAGSEXEXXKXKXEXLXSSLYDCRCRGMKREKEXXCLTYWGXHXKXGX 135
 116 LBSPEP--VNSRLSDIFPAVPIISVFOQVEHISGNCCDAKACNLDTCCKYRSY 174
 136 LEXSPEPVTSLSDIFEXXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 195
 175 ITPCTSMNS--EVCNRKCHKALROFDPKVPKHSYGMFCSCR--DIACTEBRQTIYP 231
 196 IXXCXKX 255
 232 VCSYEERPNCLSLDSCRTNYICRSLADEFTNCQPSRSVSNCKENYADCLAYSG 291
 256 SCSEYEXKPNCLDLXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 315
 292 LGTWTPTWVYVSS--SLK--VAPWCOSNSGNDLECLKFLNFKNTCLKNAIOAFNGS 349
 316 LGTMTPTWVYVSS--SLK--VAPWCOSNSGNDLECLKFLNFKNTCLKNAIOAFNGS 375
 350 DVTMMQPA--P--PVQTTATTTTAFRVRNKP--LGPAGSENE--IPTHVLP--PCANLOAQKL 403
 376 XXXXXXXXXKX 435
 404 KSNVSGSTHLCISDSDGKGLAGASSHTTKSMAPSCSLSLPVLMTALALLS 461
 436 KXNXXEXXKX 493

RESULT 2
 AC NRR1_HUMAN STANDARD: PRT: 464 AA.
 AC 000451;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEUTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNF-BETA).
 OS GFRA2 OR GDNFRB OR TRNR2.
 OS HOMO SAPIENS (HUMAN).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 97325791.
 RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA HEUCKENOTH R.O., KECK C.L., ZIMONIC D.B., POPESCU N.C.,
 RA JOHNSON E.M., JR., MILBRANDT J.;
 CC -1- FUNCTION: RECEPTOR FOR NEUTURIN. MEDIATES THE NTRN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR ALSO
 CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
 CC SPLICING IN BOTH BRAIN AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 CC EMBL: AF002700; G2145080; --.
 DR MM; 601956; --.
 DR RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
 KW ALTERNATIVE SPLICING.
 FT SIGNAL 1 21
 FT CHAIN 22 444
 FT PROPEP 445 464
 FT CARBOHYD 52 52
 FT CARBOHYD 357 357
 FT CARBOHYD 413 413
 FT LIPID 444 444
 FT VANSPLC 14 146
 SQ SEQUENCE 464 AA; 51558 MW; 3C74BBFB CRC32;

Query Match 76.5%; Score 1788; DB 1; Length 464;
 Best Local Similarity 56.2%; Pred. No. 0.00e+00;
 Matches 262; Conservative 17; Mismatches 166; Indels 21; Gaps 9;

19 SLAPSSLOGBELHGM--RPVDCVANELCAEBSNCSRYTTLRQCLAGRDNTMLAN-K 76
 24 ALPLXLLQGLGELXRLXDXCVAXXXCAEXXCSXXYTLRQCAAGXXNXXLXSGX 83
 77 E-----QALFVLOEPLDCKCRGMKREKELDCLQIYNSIHGLGEGEFYASPEP 130
 84 EXXKX 143
 131 -VTSRLSDIFRSLAFSGTGADPVYSAKSNHCLDAKACNLDNDCKLRSSISICNREI 189
 144 XVTSLSDIFRSLAFSGTGADPVYSAKSNHCLDAKACNLDNDCKLRSSISICNREI 203
 190 SPTERCNRKCHKALROFDPKVPKHSYGMFCSCR--DOACABRRQTIYSPSCYEDKE 247
 204 SXHCNRKCHKALROFDPKVPKHSYGMFCSCR--DOACABRRQTIYSPSCYEDKE 263
 248 KPNCLDLRGVORTDLCSRLADFNANCRASYQVYTGCPADNYOACLSYAGMIGFDMTP 307
 264 KPNCLDLRGVORTDLCSRLADFNANCRASYQVYTGCPADNYOACLSYAGMIGFDMTP 323
 308 NYVDSPTGIVYSPWCSGRSGNMECEKEFLRFTENPCLRNAIOAFNGCTDVNVPKG 367
 324 NYVDSPTGIVYSPWCSGRSGNMECEKEFLRFTENPCLRNAIOAFNGCTDVNVPKG 383
 368 --PSF-----QA--TOAPRVEKTPSLPDDLSDTSLGTSVITCTSVQEOGLKANSKEL 415
 384 XXPFSVXXXXXXXTXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 443
 419 SMCTELTNTIIPGSNKVIKNSGPRARRPSALITVSVLMKCAL 464
 444 XXCPELTNTIIPGSNKVIKNSGPRARRPSALITVSVLMKCAL 488

RESULT 3
 ID NRR1_MOUSE STANDARD: PRT: 463 AA.
 AC 008842;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEUTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNF-BETA).
 OS GFRA2 OR GDNFRB OR TRNR2.
 OS MUS MUSCULUS (MOUSE).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 97325791.
 RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

ID	GENE	SEQUENCE	START	END	SCORE	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	
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[illegible]

ID	GNDR HUMAN	STANDARD:	PRT:	464 AA.
AC	P56159			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	GNDR RECEPTOR ALPHA PRECURSOR (GNDR-ALPHA) (TGF-BETA RELATED			
DE	NEUROTROPIC FACTOR RECEPTOR 1).			
GN	GFRL OR GDNFR OR TRNR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARIOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:			
OC	EUTHERIA: PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-SUBSTANTIA NIGRA:			
RX	MEDLINE: 96270513.			
RA	JING S., WEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMIR R.,			
RA	ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,			
RL	FOX G.M.;			
CC	CELL 85:113-1124(1996).			
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED			
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY			
CC	SIMILARITY).			
CC	-1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX			
CC	WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY			
CC	SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY			
CC	SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.			
DR	MIM: 601496; -			
CC	RECEPTOR: GLYCOPROTEIN: GPI-ANCHOR; MEMBRANE; SIGNAL.			
KW	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	425	428	GDNF RECEPTOR ALPHA.
FT	PROPEP	429	464	HYDROPHOBIC, REMOVED DURING MATURATION
FT				(POTENTIAL).
FT	DOMAIN	361	368	POLY-THR.
FT	CARBOHYD	59	59	POTENTIAL.
FT	CARBOHYD	346	346	POTENTIAL.
FT	CARBOHYD	405	405	POTENTIAL.
FT	LIPID	428	428	GPI-ANCHOR (POTENTIAL).
SO	SEQUENCE	464 AA:	51291 MM:	268C3574 CRC32:
	Query Match	75.2%	Score 1758:	DB 1: Length 464:
	Best Local Similarity	52.6%:	Pred. No. 0.00e+00:	
	Matches 254: Conservative	24:	Mismatches 186:	Indels 19: Gaps 14,
Db	1 MFLATLVALPDLDDLLEAEVSGGDR--DVKASDGLKQSGSSTKRTLRQCVAKRET	58		
Y	16 MFLATLVALPDLLEAEVSGGDR--DVKASDGLKQSGSSTKRTLRQCVAKRET	75		
Db	59 NFSLASGLAEAD--CRGAMALNOKSLYCRCKRGKMKENCLRIYWSMTQSQ--GNDL	115		
Oy	76 NTLXASGEXXXXXXXAXAXEXLXSSSLYDRCRRGKMKEXCLXIYWSMXLXAXGNX	135		
Db	116 LEDSYEP-VNSRLSDIRRVVPIISDVFOQVEHPIKGNMCLDAKACNLDDICKKYSAY	174		
Oy	136 LEXSPYEPXVTSRLSDIRRXSXXXXXXDXXXXXXKSMXCIDAAKACNLDDICKKLSAY	195		
Db	175 ITPCTYSN-DVCRRRRCHALNOKFDPKVAKSYGLFPCSCR--DIACERRRRTIP	231		
Oy	196 IAXCXXXXXXEKRNRCHALNOKFDPKVAKSYGLFPCSCR--DIACERRRRTIP	255		
Db	232 VCSYEEREPNCL-LDSCKTNYICRSLADFTHNCOPESTRSVSSCLKENYADCLLAYS	290		
Oy	256 SCSEYEXEKPCPLDRXXCFTDXLCRSLADFTHNCKXXXXXXKXVASCAXNYXKLAXYG	315		
Db	291 LIGIVMPNYIDSS-SLS-VAPWCDGNSGNDLECLFLNFFDNTCLANAIOFNGS	348		
Oy	316 LIGIXMTPNYIDSSYTXXXVAPWCDGNSGNSXEECEKFLFFXXNCLANAIOFNGX	375		
Db	349 DVTWQPA--P--VQQTATTTTALRVKNRP--LGPAGSENE--LPTVLVPPCANLQX	402		
Oy	376 XXXXXXXXXKXFEVXXXXXXXTXIAKRXKXPSLXXXXXXKXIXTXVXXCXKLQX	435		

Dd	403	KSNVSGNHLCLISN-GNTEKEBGLASSHTTTSSMAAPPSCGISPLVLVTALSTLSLT	461
Oy	436	KKNKSKSXKKXCPXYELTNTNNXXXSGXXXXXXSXXAXPSKALXLPLMLTALAILTSXX	495
Dd	462	ETS 464	
Oy	496	XKS 498	

RESULT	6		
ID	GDNF_CHICK	STANDARD:	PRT: 469 AA.
AC	013156:		
Dt	01-NOV-1997 (REL. 35, CREATED)		
Dt	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)		
Dt	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)		
DE	GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).		
GN	GFPAL OR GDNFRA		
OS	GALLUS GALLUS (CHICKEN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHIA; GALIIFORMES.		
OC	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE-BRAIN:		
RC	BUTBELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSENTHAL A., CHINCHEIRO M., BUCHMAN V.L., DAVIES A.M.; NATURE 387:721-724(1997).		
RL	NATURE 387:721-724(1997).		
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY SIMILARITY).		
CC	-1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF GPI (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.		
DR	EMBL: U90541: G2213803; --		
KW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.		
FT	SIGNAL 1 27 POTENTIAL.		
FT	CHAIN 28 430 GDNF RECEPTOR ALPHA.		
FT	PROPEP 431 469 HYDROPHOBIC, REMOVED DURING MATURATION (POTENTIAL).		
FT	DOMAIN 361 368 POLY-TIR.		
FT	CARBOHYD 62 62 POTENTIAL.		
FT	CARBOHYD 163 163 POTENTIAL.		
FT	CARBOHYD 346 346 POTENTIAL.		
FT	CARBOHYD 405 405 POTENTIAL.		
FT	LIPID 430 430 GPI-ANCHOR (POTENTIAL).		
SO	SEQUENCE 469 AA: 52043 MW: C6D2A1C9 CRC32:		

Query Match	68.4%;	Score 1599;	DB 1;	Length 469;
Best Local Similarity	49.3%;	Pred. NO. 0.00e+00;		
Matches 237;	Conservative 31;	Mismatches 189;	Indels 24;	Gaps 17

Dd	1	MFLALITLADLPADVLSAEVSGLPGRDLDCVVASDCLKEOSCSRYRFTLRQCVAGKE	60
Oy	16	MKLXLSTLAPLPLXXHLGGAELEGXKXRLLX--DCVAXXXXCXKEXXCXYYRTLROCKAGGX	74
Dd	61	SNFSAATGLEAKDE--CKSAMELAKOKSLYNCRCKRGKKKCNCLRITYMSYQLQ--GND	117
Oy	75	XNTXLASGXEXXXXXXXCAAXEKLXSSLVDCCRKRGMKKEKXCLXTIWSYHXLYLGXNX	134
Dd	118	LLEDSPYEP--VNSRLSDIFRLAPIVS---EPVLS-KGNNCCLDAKACNLDTCKRRPSA	172
Oy	135	XLESAPYEPXYTSLSDLFRIKXSXXSXXKXMXKXKXSNKCLDAKACNLNDCKRLRSA	194
Dd	173	YTTPCTSTSN-EICNRKRCHKALRLFEDKYVPRHYSYGLMFCSCR--DVACTERRQTV	229
Oy	195	YIXXCXXXXXXEXERCNRKRCHKALRFQFDKVPXHHYXGLMFCSCHXXDXACXERRQTI	254
Dd	230	PVCSEYDERERNCLNDOESCCKNYICGSRLADFTTNQPESRSYSSCLKENYADCLAYS	269
Oy	255	PCSEEXEKERNCLDRXCRTDLCBSRLADFTTNCXXXXRXVSCXAXNXXCCLAAYX	314

Dd	290	GILGIVMPNPNYIDSS-SIS-VAPMCDCNSNDIDECKRFNFQDWTCLKNAIOAFNG	347
Oy	315	GILGIXMTFNPVDSXITXXVAPMPCXCGSGNXEBCERFLAETFXNPPCLNMAIOAFNG	374
Dd	348	TDVNWQ----PILEVOITTAATTATASHLKNKG-ETTNEIPT-HND-SPACANIQAOK	400
Oy	375	XXXXXXXXXXXXPXFVXXXXXXXXXTYAXRVXXXXPSLXXXXXXLLXTLVXXXCCXXLOXQ	434
Dd	401	KRKSSEVDTELCENEMNIGKDNTPGVSTHISSENALPTSYPTPLIMTIALSLF	460
Oy	435	L-KNKRKSKXXXXCFEXELTTNNXXXXSGXXXX-IXXXXXXAPXSMALXXLP-VLMUTLALXL	491
Dd	461	I	
Oy	492	L	492
RESULT	7	STANDARD:	PRT: 465 AA.
ID	NRRR-CHICK		
AC	013157:		
DT	01-NOV-1997 (REL. 35, CREATED)		
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)		
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)		
DE	NEURTRIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GNDF		
DN	RECEPTOR BETA) (GDNR-BETA).		
GN	GFRA2 OR GDNFRB.		
OS	GALLUS GALLUS (CHICKEN).		
OC	EUDARIOTIA METAZOIA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;		
OC	GALLIFORMES.		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-BRAIN:		
RA	BUJ-BELO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,		
RA	ROSENTHAL A., CHINCHEITU M., BUCHMAN V.L., DAVIES A.M.;		
RL	NATURE 387:721-724(1997).		
CC	-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED		
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE		
CC	TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE		
CC	RECEPTOR (BY SIMILARITY).		
CC	-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.		
CC	-I- SIMILARITY: BELONGS TO THE GDNFR FAMILY.		
DR	EMBL: U90542; G2213805; -		
KW	RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.		
FT	SIGNAL	1	21
FT	CHAIN	22	445
FT	PROPEP	446	465
FT	CARBOHYD	355	355
FT	CARBOHYD	387	387
FT	CARBOHYD	412	412
FT	LIPID	445	445
SO	SEQUENCE	465 AA;	51908 MW; 5CA073B4 CRC32;
Query Match	66.8%;	Score 1561;	DB 1; Length 465;
Best Local Similarity	47.8%;	Pred. No. 0.00e+00;	
Matches	223;	Conservative 44;	Mismatches 177; Indels 23; Gaps 122
Dd	19	SLAAPSPPGDLOGW-RVPVDCIFANLKCAEAGSCSRYYTLNQCLAGPRRNTMLAN-K	76
Oy	24	ALPLTXLLQGAELMKXMXKLXDVCVYAXXXCAEXXCXSXYTYTLNQCANAXXNXTXLSGX	83
Dd	77	E-----COALEVIEQESPILDRCRKCRMRKEIOCLOYVYSIHGLAGEEFYEASPREP	130
Oy	84	EXKXXXXKXKAEXELKXSSTLDCCRKRGMKKEXCLATYNSKHXKXLLXGNAXLEXSPREP	143
Dd	131	-ITSRLSDIFRLASIFSGM--DPATNSKSNHC LDAAKACNLDNCKRLRSYGISTCSKEI	187
Oy	144	XVTSRLSDIFRXSXSSXXXXXDXKXKXSNXCLDAFAKCNDLNDXCKRLRSAYIXXXCXXX	203
Dd	188	SATESCRRKCKHALROFFDVNPVSRYTRLRFLCGRK--DOACAEPRTQIYPFGSYEDEKE	245
Oy	204	SXKERCNRRKCKHALROFFDVNPXHXHGMFLCSGXKXADKXERRRQTITPSCSYEXXE	263

ID	NOTCH_XENLA	STANDARD	PRT	2524 AA.
AC	P21783:			
DT	01-MAY-1991 (REL. 18, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (NOTCH PROTEIN).			
GN	XOTCH.			
OS	XENOPUS LAEVIS (AFRICAN CLAWED FROG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	COFFMAN C., HARRIS W., KINTNER C.;			
RA	MEFLINE; 90385285.			
RL	SCIENCE 249:1438-1441(1990).			
RN	[2]			
RP	REVISIONS TO 1759-1782.			
RA	KINTNER C.;			
RL	SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC	-1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.			
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.			
CC	-1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.			
CC	-1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.			
CC	-1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.			
CC	-1- SIMILARITY: CONTAINS 6 ANK REPEATS.			
DR	EMBL; M33874; G1364263;			
DR	PIR; A35844; A35844.			
DR	HSP; P20693; 1EST.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 23.			
DR	PROSITE; PS00022; EGF_1; 34.			
DR	PROSITE; PS01186; EGF_2; 29.			
DR	PROSITE; PS01187; EGF_CA; 21.			
KW	DIFFERENTIATION; NEUROGENESIS; REPEAT; ANK REPEAT; EGF-LIKE DOMAIN;			
KW	TRANSMEMBRANE; SIGNAL; GLYCOPROTEIN.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	2524	NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG.
FT	DOMAIN	20	1728	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1729	1750	POTENTIAL.
FT	DOMAIN	1751	2524	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	20	57	EGF-LIKE 1.
FT	DOMAIN	38	99	EGF-LIKE 2.
FT	DOMAIN	102	140	EGF-LIKE 3.
FT	DOMAIN	141	177	EGF-LIKE 4.
FT	DOMAIN	179	215	EGF-LIKE 5.
FT	DOMAIN	217	254	EGF-LIKE 6.
FT	DOMAIN	256	292	EGF-LIKE 7.
FT	DOMAIN	294	332	EGF-LIKE 8.
FT	DOMAIN	334	370	EGF-LIKE 9.
FT	DOMAIN	371	409	EGF-LIKE 10.
FT	DOMAIN	411	449	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	451	487	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	489	525	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	527	563	EGF-LIKE 14.
FT	DOMAIN	565	600	EGF-LIKE 15.
FT	DOMAIN	602	638	EGF-LIKE 16.

FT	DISULFID	644	654	BY SIMILARITY.
FT	DISULFID	649	663	BY SIMILARITY.
FT	DISULFID	665	674	BY SIMILARITY.
FT	DISULFID	681	692	BY SIMILARITY.
FT	DISULFID	686	701	BY SIMILARITY.
FT	DISULFID	703	712	BY SIMILARITY.
FT	DISULFID	719	729	BY SIMILARITY.
FT	DISULFID	724	738	BY SIMILARITY.
FT	DISULFID	740	749	BY SIMILARITY.
FT	DISULFID	756	767	BY SIMILARITY.
FT	DISULFID	761	776	BY SIMILARITY.
FT	DISULFID	778	787	BY SIMILARITY.
FT	DISULFID	794	805	BY SIMILARITY.
FT	DISULFID	799	814	BY SIMILARITY.
FT	DISULFID	816	825	BY SIMILARITY.
FT	DISULFID	832	843	BY SIMILARITY.
FT	DISULFID	837	854	BY SIMILARITY.
FT	DISULFID	856	865	BY SIMILARITY.
FT	DISULFID	872	883	BY SIMILARITY.
FT	DISULFID	877	892	BY SIMILARITY.
FT	DISULFID	894	903	BY SIMILARITY.
FT	DISULFID	910	921	BY SIMILARITY.
FT	DISULFID	915	930	BY SIMILARITY.
FT	DISULFID	932	941	BY SIMILARITY.
FT	DISULFID	966	997	BY SIMILARITY.
FT	DISULFID	991	1006	BY SIMILARITY.
FT	DISULFID	1008	1017	BY SIMILARITY.
FT	DISULFID	1024	1035	BY SIMILARITY.
FT	DISULFID	1029	1044	BY SIMILARITY.
FT	DISULFID	1046	1055	BY SIMILARITY.
FT	DISULFID	1062	1073	BY SIMILARITY.
FT	DISULFID	1067	1082	BY SIMILARITY.
FT	DISULFID	1084	1093	BY SIMILARITY.
FT	DISULFID	1100	1121	BY SIMILARITY.
FT	DISULFID	1115	1130	BY SIMILARITY.
FT	DISULFID	1132	1141	BY SIMILARITY.
FT	DISULFID	1148	1159	BY SIMILARITY.
FT	DISULFID	1153	1168	BY SIMILARITY.
FT	DISULFID	1170	1179	BY SIMILARITY.
FT	DISULFID	1186	1197	BY SIMILARITY.
FT	DISULFID	1191	1206	BY SIMILARITY.
FT	DISULFID	1208	1217	BY SIMILARITY.
FT	DISULFID	1224	1243	BY SIMILARITY.
FT	DISULFID	1237	1252	BY SIMILARITY.
FT	DISULFID	1254	1263	BY SIMILARITY.
FT	DISULFID	1270	1283	BY SIMILARITY.
FT	DISULFID	1275	1292	BY SIMILARITY.
FT	DISULFID	1284	1303	BY SIMILARITY.
FT	DISULFID	1310	1321	BY SIMILARITY.
FT	DISULFID	1315	1331	BY SIMILARITY.
FT	DISULFID	1335	1344	BY SIMILARITY.
FT	DISULFID	1351	1362	BY SIMILARITY.
FT	DISULFID	1356	1371	BY SIMILARITY.
FT	DISULFID	1373	1382	BY SIMILARITY.
FT	DISULFID	1390	1401	BY SIMILARITY.
FT	DISULFID	1395	1412	BY SIMILARITY.
FT	DISULFID	1414	1423	BY SIMILARITY.
FT	CARBOHYD	462	462	POTENTIAL.
FT	CARBOHYD	887	887	POTENTIAL.
FT	CARBOHYD	958	958	POTENTIAL.
FT	CARBOHYD	1178	1178	POTENTIAL.
FT	CARBOHYD	1487	1487	POTENTIAL.
FT	CARBOHYD	1508	1508	POTENTIAL.
FT	CARBOHYD	1584	1584	POTENTIAL.
SO	SEQUENCE	2524 AA;	275123 MW; E63584B1 CRC32;	
Query Match	Similarity	4.6%;	Score 108; DB 1; Length 2524;	
Best Local	Similarity	15.2%;	Pred. No. 6.55e-04;	
Matches	25; Conservative	21; Mismatches	108; Indels 10; Gaps 1;	
Db	1149	SPNFCNGATCTDVLGGSCCVAGYHGVCN-SEINECGSHPNQNGSTCIDLNTYKCS	1307	
49	AXXXGXXARXXGXXSYVPTB-OTVYGCXXVXXNMTJASCCXXVXX			

Query Match 85.1%; Score 1781; DB 1; Length 463;
 Best Local Similarity 54.0%; Pred. No. 0.00e+00;
 Matches 248; Conservative 10; Mismatches 188; Indels 13; Gaps 4;

DB 16 TLRSLASPSSPGSGELHGRPOVDVAVNELCAASNCSSRYRTLRQCLAGDRMTML-- 73
 17 TLXSLXPLXLLXSSXXSXKXDCVAXXCAEXXCSXXRTLRQCLAGDRMTML-- 76
 74 ---ANKCOALAEVQESLYDCCRCKRGKKELOCLQIYWSHLGLTBESEYEASPIE- 129
 77 XXXAXXECXAXEXLXSSLYDCCRCKRGKKELOCLQIYWSHLGLTBESEYEASPIE- 136
 DB 130 PVTSLRSLDIFRLASIFSGGADPVVSAKSNHCLDAKACNLNDNCKRLSSYISICNMEI 189
 137 PVTSLRSLDIFRLASIFSGGADPVVSAKSNHCLDAKACNLNDNCKRLSSYISICNMEI 196
 DB 190 SPTECRNRKCKHAKALROFEDRVPSSEYTYRMLFCSCQ--DQACERRROTILPSCSYEDKE 247
 197 SXEXERCNRKCKHAKALROFEDRVPSSEYTYRMLFCSCQ--DQACERRROTILPSCSYEDKE 256
 DB 248 KNCCLDLRLCTDHLGSRDLADFHANCASTRITSCPADNYOACLSYAGMIGFDMTP 307
 257 XNCLDLRLCTDHLGSRDLADFHANCASTRITSCPADNYOACLSYAGMIGFDMTP 316
 DB 308 NYVDSNPTGIVVSPMNCRCRSGNMECEKFLKDFTEPNCLNATOANGNDVAMSPRG 367
 317 NYVDSNPTGIVVSPMNCRCRSGNMECEKFLKDFTEPNCLNATOANGNDVAMSPRG 376
 DB 368 PTFSAQAP----RVEKTPSLPDDLSDTSLGTSVITTCSTIQDQKANNKELSMCF 422
 377 PXXXTXAXXAXXAXXHXVXXPLXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXX 436
 DB 433 TELTINISPGSKVYKIXSGCRALSTALTAPLMT 461
 437 XXXXXXXXXXXXXXXXXXXXXXXXAXXAXXAXXAXXAXXAXXAXXAXXAXX 475

RESULT 2 STANDARD: PRT: 468 AA.

ID GDNF-RAT
 AC 062997;
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (GDF-BETA RELATED
 DE NEUROTHROPIC FACTOR RECEPTOR 1) (RET LIGAND 1).
 DE GDFAL OR GDNFRA OR TRNRI OR RETLI.
 DE RATIUS NORVEGICUS (RAT).
 DE EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 DE EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-KIDNEY;
 RX MEDLINE: 96270513.
 RA JING S., WEN D., YU Y., HOLST P.-L., LUO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTROCK B.W.,
 RA FOX G.M.;
 RA CELL 85:1113-1124(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-KIDNEY;
 RX MEDLINE: 973232356.
 RA SANICOLA M., HESSION C.A., MORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA MAUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PERINSKY R.B., CATE R.L.;
 RA PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-KIDNEY;
 RX MEDLINE: 96273032.
 RA TREANOR J.J.S., GOOGMAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,
 RA BECK C.D., GRAY C., ARANANT M.P., POLLOCK R.A., HETTI F.,
 RA PHILLIPS H.S., GODDARD A., MOORE M.W., BUJ-BELLO A., DAVIES A.M.,
 RA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;

RL NATURE 382:80-83(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: U59486; G139863; -
 DR EMBL: U97142; G282022; -
 KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 430
 FT PROPEP 431 468
 FT DOMAIN 362 369
 FT CARBOHYD 59 59
 FT CARBOHYD 347 347
 FT CARBOHYD 406 406
 FT LIPID 430 430
 SO SEQUENCE 468 AA; 51649 MW; 6A7A2B2A CRC32;

Query Match 85.0%; Score 1779; DB 1; Length 468;
 Best Local Similarity 50.7%; Pred. No. 0.00e+00;
 Matches 241; Conservative 12; Mismatches 213; Indels 9; Gaps 8;

DB 3 LATYFALPLDLILMSAEVSGGDRDCVKASDCLKQSCSTYRRLRQCVAGKETNFSL 62
 15 LXTLSLXPLXLLXSSXXSXKXDCVAXXCAEXXCSXXRTLRQCLAGDRMTML-- 74
 DB 63 TSGLEANDCRSANEALOKSLYNCRCRCKRGKKELOCLQIYWSHLGLTBESEYEASPIE 121
 75 XXXAXXECXAXEXLXSSLYDCCRCKRGKKELOCLQIYWSHLGLTBESEYEASPIE 134
 DB 122 E-PVNSRLSDIFRAVPIPSDVOVEHISGNKNCCLDAKACNLNDNCKRLSSYISICNMEI 180
 135 EXPVTSRLSDIFRAVPIPSDVOVEHISGNKNCCLDAKACNLNDNCKRLSSYISICNMEI 194
 DB 181 SMSN-EVCNRRKCKHAKALROFEDRVPAKSYGMLFCSCQ--DIACERRROTILPSCSYED 237
 195 SXEXERCNRKCKHAKALROFEDRVPAKSYGMLFCSCQ--DIACERRROTILPSCSYED 254
 DB 238 RERNCLSDLOSKTNYICRSLADFTNCPQPSRSVSNCKENYADCLLAYSGLIGTVM 297
 255 XEAPNCLDLXSKRTDLCRSLADFTNCPQPSRSVSNCKENYADCLLAYSGLIGTVM 314
 DB 298 TPNTVDS-SLS-VAPWCDSCNSGNDLEDCLEFNFKDTCLKNAIOAFNGSDVTMNO 355
 315 TPNTVDSXAXXAXXVAPWCDSCNSGNDLEDCLEFNFKDTCLKNAIOAFNGSDVTMNO 374
 DB 356 PAPPVOTTTATTTAFRVRNKP-LGPAGSENEIP-THVLPPCANLQAKLSNVSGSTHL 413
 375 XXPVOTTTATTTAFRVRNKP-LGPAGSENEIP-THVLPPCANLQAKLSNVSGSTHL 434
 DB 414 CLSDSDRGKGLAGASHTTKEMAPRSCSLSLVLMITLALALLSVLATS 468
 435 CXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXX 489

RESULT 3 STANDARD: PRT: 464 AA.

ID NTRR-HUMAN
 AC 000451;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEUTRIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTHROPIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNFR-BETA).
 DE GFR2 OR GDNFRB OR TRNR2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]

ID	GNDR	MOUSE	STANDARD:	PRT:	468 AA.
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)			

Query Match	84.2%	Score 1762;	DB 1;	Length 468;
Best Local Similarity	49.7%	Pred. No. 0.00e+00;		
Matches 226;	Conservative 19;	Mismatches 211;	Indels 9;	Gaps:
Db	3	LATLFFVLPLDLLMSAEVSGGRLDLCVKASDQCLKEOSCTRYRTLROCVAGKETNFSL	62	
Qy	15	LXTLXLXPLXLLKXSSXXXXXXDCVAXXXCMAEXKXSXXYRTLROCGAXGXXNXXX	74	
Db	63	TSGLEAKDECSAMEBALKQNSLYICRCKRGKKEKNCRLRTYMSYOSLO-GNDLLEDSPT	121	
Qy	75	XXXXXXAXXECXXAXEXLXSLYDRCRCRCKREKEXCLXIYWSYHXXLXXGXXLXESPY	134	
Db	122	E-PVNSRLSDIEFRAVPIISDFQOEVIHSIGNNCILDAKACNLDDPTCKYRSAYITPCTT	180	
Qy	135	EXPTSRISDIEFRXSSXXSXXKXDXKXSSXXSNCLDAKACNLDDCKRLRSATIXXXCX	194	
Db	181	SMSN-EVCNRRKCKAKALROEFDDKPAKHSYGMFLFCSCR--DVACTERRROTIVPVCSE	237	
Qy	195	XXSXHEGNCNRKCKAKALROFEDKPYAHXXYGMFLFCSCXXDXMACXERRROTIVPSCYEX	254	
Db	238	REPNCNLADSCSTNYICNSRLADFTTNCQPESSRSVSNCLKENYADCLLAYSGLIGTVM	297	
Qy	255	XEXENCLDLRSXCRTDLKSLRLADFTTNCXPXXRYTXCXANRYXXCLAYXGLIGTGM	314	
Db	298	TPNTIDSS-SLS-VAPNCDGNSGNDLEDCLKFLNFKNQNTCLKNAIOATGNGSDVTMMQ	355	
Qy	315	TPNTVDSXXYXXVAPNCCXRGSGNXXEDECFLXKXNXPCLNLAIOATGNGSDVXMSQ	374	
Db	356	PAPVQTTATMTAFRIKNRP-IGPAGSENEIP-TVLPPCANLQAKLKSNVSGSTHL	413	
Qy	375	XXPXXXXTXAXXXXXXXVXXPKLAXXXSXXXXXXXTYXXXCXXOXOLKXNXXSXXXX	434	
Db	414	CLSDNDYGRDGLAGASSHTTKSMAAPSPCGSLSLPVMEFTALAAALLSVSLAETS	468	
Qy	435	CXXXXXXSXXXXXXSXXXXXXSXXAXXXSXXLXLPLMLTLTXLXXLXLXLETSS	489	

ID	GDNF_HUMAN	STANDARD:	PRT:	464 AA.
Dt	P56159			
Dt	01-NOV-1997 (REL. 35, CREATED)			
Dt	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
Dt	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
De	GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).			
OS	GPRAL OR GDNFRA OR TRNRI.			
GN	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES.			
Rn	[1]			
Rc	SEQUENCE FROM N.A.			
Rc	TISSUE-SUBSTANTIA NIGRA:			
Rx	MEDLINE: 96270513.			
Ra	JING S., WEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMIR R.,			
Ra	ANTONIO L., HU Z., COPPLES R., LOUIS J.-C., HU S., ALTRICK B.W.,			
RA	FOX G.M.;			
CC	CELL 85:1113-1124(1996).			
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY SIMILARITY).			
CC	-1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).			
Cc	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.			
Km	MIM: 601496.			
Dk	RECEPTOR GLYCOPROTEIN: GPI-ANCHOR; MEMBRANE; SIGNAL.			
Ft	SIGNAL 1 24 POTENTIAL.			
Ft	CHAIN 25 428 GDNF RECEPTOR ALPHA.			
Ft	PROPEP 429 464 HYDROPHOBIC. REMOVED DURING MATURATION (POTENTIAL).			
Ft	DOMAIN 361 368 POLY-THR.			
Ft	CARBOHYD 59 59 POTENTIAL.			
Ft	CARBOHYD 346 346 POTENTIAL.			
Ft	CARBOHYD 405 405 POTENTIAL.			
LIPID	428 428 GPI-ANCHOR (POTENTIAL).			
SQ	SEQUENCE 464 AA: 51291 MW; 2683574 CRC32;			
Query Match	81.1%; Score 1696; DB 1; Length 464;			
Best Local Similarity	49.7%; Pred. No. 0.00e+00;			
Matches 236:	Conservative 16; Mismatches 210; Indels 13; Gaps 11.			
Db	3 LATVIALPLDLLLSAEVSGGDRLDYKASQQCLKEGSCGRVTTLAQCAGETNSFL 62			
y	15 KATLSLKXPKLLSXSSXXXXXXXXXXDCYAAXXXXCAEXXSXYITRLOCKAGXXXXX 74			
Db	63 ASGLEAKDECSRAMEALKOKSLYNCRCKRGMKRNKNCLRIYWSTYOQL -GNLDLESDPY 121			
Oy	75 XXXXXXXXCXAXEKELXSSSLYDRCRKRMKKEXXCLXIYWSHXKLXGXKXLEXSPY 134			
Db	122 E-PVMSRLSDIFRRVPFTISDVYGOVEHLPRKGNCLDAKAACNLDDICKRSAYITPCTT 180			
Oy	135 EXPVTSRLSDIFRXKSXSSXXXXXKSNKCILDAAKACLNDCKRKSAYIIXCX 194			
Db	181 SVSN-DVCNRKRCHKALRFQFDKPVAFKSHSYMLFCSCR--DIACTERRORTIVPVCSYE 237			
Oy	195 XHSXRHCRRCHKALNQFFDKVPMXMYGLMTCSCAXXDAXEERRORIIPSCGYEX 254			
Db	238 RKPNCL-LDSCKNTNYICSRSLADFTTNCPESRSVSCLKENYADVCLLAYSGLTGM 296			
Oy	255 XEPNCIDLRSKCDTXLCBSRLADFXTNCPXPYYXTYXCXANYYXXCLAAYXGLGTGM 314			
Db	297 TPNTIDSS-SLS-VAPWDDCGSNSNDLEECLEFLNFERNDTCLKNAIQAFNGSDVTWM 354			
Oy	315 TPNIYDS.XXTXXXXAAMPWCXCRGSNGMXEECEKFLLXXNXNPCLMAIQAFNGSDXVM 374			
Db	355 PAPVOYTATTATTLARKNKRP-GDPAGESENEIP-TVLPPCANTLAOKTKSVSGHTIH 412			
Oy	375 XXPXXXXXXJXXXXXXXRPXXXXPLXXXXXXXKXXXTVVYXXKXDXOXOLKXNXXSKXXX 434			

Dd	413	CISGNENRKGGLASSHIITK-SMAPRPGCSPLVLYVTALSTLLS--LTETS	464
Oy	435	CAAXXXXXXXXXXXXXXXXSXAXXSXLLXLPVLMTLTXLXXLXXLXTETS	489
RESULT	6	STANDARD:	PRT: 465 AA.
ID	NTRR.CHICK		
AC	013157;		
Dt	01-NOV-1997 (REL. 35, CREATED)		
Dt	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)		
Dt	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)		
Dt	NEURINURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRNR-ALPHA) (GDNF RECEPTOR BETA) (GDNFR-BETA).		
Gn	GFRA4 OR GDNFRB.		
Os	GALLUS GALLUS (CHICKEN)		
Oc	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHA		
Rn	GALLIFORMES.		
Rn	(1)		
Rc	SEQUENCE FROM N.A.		
Rc	TISSUE=BRAIN;		
Ra	BUT-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSENTHAL A., CHINCHEIRO M., BUCHMAN V.L., DAVIES A.M.;		
Rl	NATURE 387:721-724(1997).		
Cc	-I- FUNCTION: RECEPTOR FOR NEURTIRIN. MEDIATES THE NRTN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE TO MODULATE GENE SIGNALING THROUGH THE RET TYROSINE KINASE RECEPTOR (BY SIMILARITY).		
Cc	-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.		
Cc	-I- SIMILARITY: BELONGS TO THE GDNFR FAMILY.		
Dr	EMBL: U90542; G2213805;		
Kw	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.		
Ft	SIGNAL	1	21
Ft	CHAIN	22	445
Ft	PROPEP	446	465
Ft			
Ft	CARBOHYD	355	355
Ft	CARBOHYD	387	387
Ft	CARBOHYD	412	412
Ft	LIPID	445	445
Sc	SEQUENCE	465 AA;	51908 MM; SCA073E4 CRC32;
Query Match		76.8%; Score 1607; DB 1; Length 465;	
Best Local Similarity		47.1%; Pred. No. 0.00e+00;	
Matches	218; Conservative	33; Mismatches 196; Indels 16; Gaps	
Dd	16	TLRLSLAPSPSPGGDLQGWVPVDCIRANKLCAAEGSCSSRYRTLRCOCLAGDRNTML--	73
Oy	17	TLXSLMXPFLMXLSXXXXXXRXDXCAXAXXCAEXXC SXXYRTLRCGXGXXXXXX	74
Dd	74	--ANKECOALELVLOSPLYDCCRCKGMRETOICLOVYMSHLGLAGEGEFEASPYE-	
Oy	77	XXXXXXECXAXEXLXSSSLYDCCKRGKKRKXCLTIWSHXHLXGXGXMLEKSPYN-	
Dd	130	PITSRLSDIFRLASIFSGM--DPATNSCKSNHCDAKACNLNDNCRLRSIGYSTSKEL-	
Oy	137	PVTSRLSDIFRXSXSSXXXXXXDKSSXMCDAKAKACLNDXCKKLKSATYIXKXXXX	196
Dd	188	SATHCSRRCRHARLRPFEPNVSEITTYRLFCSC--DQACEPRRQTIVFCSYEDEK	245
Oy	197	SXXSRCNRRRCRHARLRPFEPKVXHXHYGLFCSCXXXDACXERRRQITXPSCSYEXE	256
Dd	246	KPNCLDIRNYCARADHLCRSLADFHANCGASFSLSCSGDVNYOACLGSYTGLIGEDMP	305
Oy	257	XPNCLDIRSKCRFDXLCLRSFLADFPXNCAPXKXKXKXCAKNYKXCLANVXGLIGTGMTP	316
Dd	306	NYVDASTTSTITISPCSCSKSGNMLEEECEKFLDFEFENCLNNALOAFNGTDVNLSPKN	365
Oy	317	NYVDSTTTXVVAVPWCKGRSSGNXKECEKFLXKFAYNCCLANALOAFNGNDVAMSOXX	376
Dd	366	PSPPTTM-LPKYEKSPALPD-DINDSNTMYD-TSITTTCTSIQEHGOKLNKSKESOLCY	421
Oy	377	PXXXXXTAXXXXXXXRVXXXPYLKXXXXXXXXXXXXYYXXCXKXOXOXLKXNXSXXXXXC	436

DB 422 SETQLTDMPOKTFVDOKAAGSRHRAARILPAVPLIKL 464
 QY 437 XXXXXXXXXXXXXXXXXXXXXXXXXX-5XXXLXPLVLLTLX 477

RESULT 7
 ID GDNF CHICK STANDARD: PRT: 469 AA.
 AC 013156;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFR.
 OS GALUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BOU-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSENTHAL A., CHINCETRU M., BUCHMAN V.L., DAVIES A.M.;
 RL NATURE 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: U90541; G2213803; -
 KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 27
 FT CHAIN 28 430
 FT PROPEP 431 469
 FT DOMAIN 361 368
 FT CARBOHYD 62 62
 FT CARBOHYD 163 163
 FT CARBOHYD 346 346
 FT CARBOHYD 405 405
 FT LIPID 430 430
 SQ SEQUENCE 469 AA; 52043 MM; C8D241C9 CRC32;.

Query Match 72.7%; Score 1521; DB 1; Length 469;
 Best Local Similarity 45.2%; Pred. No. 0.00e+00;
 Matches 212; Conservative 23; Mismatches 219; Indels 15; Gaps 12;

DB 6 LYLALPLADVLASVSLPBGDRLDCKYKASDOCKRESCTKRYRTLRQCAVAKESPSR 65
 QY 15 LXTLSLXPLXLLXSSXXXXXXDXVAXXXCXAEKXCSXKRTTLQCAAGAXXKX 74

DB 66 ATGLEAKDECKSAMKALOKSLYNCRCRGMKKEKNCRIYMSYOSIQ-GNDLELSPY 124
 QY 75 XXXXXXXXECAXXEXLXSSLYDCRCRGMKKEKNCRIYMSYOSIQXXXXLESPY 134

DB 125 E-PVNSRLDIFRLAPIVSV---EPVLS-KNNCLDAKACNLNDTCRPSAVITPPTS 179
 QY 135 EXPVTSRLDIFRXKSSXXXXXXDXKSNXCDAKACNLNDCKRLSAVIXKXX 194

DB 180 STSN-EICNKRKCHALFLFDKVPKRHSYGMTCSCSR--DVACERRORTIVPCSYED 236
 QY 195 XXXXKERNRRKCHALQFFDKVPKHXHXYGLFSCXXXDXACKERRORTIVPCSYEX 254

DB 237 REKPCNLIOESCKKNYICRSRLADFTNCOPEHSRSVSSCKENYADCLAYSGILGTVM 296
 QY 255 XEPRCCLDRKCRDXLCLRSRLADFTNCOPEHSRSVSSCKENYADCLAYSGILGTVM 314

DB 297 TPNYIDSS-SLS-VAPWCDSCNSGNDIDECRKFLEFODNTGLKNAIDAFNGNDVYVWQ 354
 QY 315 TPNYIDSSXXTXVAPWCDSCNSGNDIDECRKFLEFODNTGLKNAIDAFNGNDVYVWQ 374

DB 355 PILVQTTATTTATTSRLKNTGSETTNEIPTHNDSPACAN-LQAKRR-KSNESVDTEL 412
 QY 375 XXPXXXXXXTAXXXXXXXRXVXXPKLXXXXSSXXXXXXITVYXXKQXKXKXNXXXXX 434

DB 413 CLNENAIGKDNTPGVSTSHISENSFALPTSFYPSPLILMTALSFL 461
 QY 435 CXXXXXXXKXXXXXXXKXXXXXXX-SXXAXXKXLLXLP-VLMLTLXLLX 481

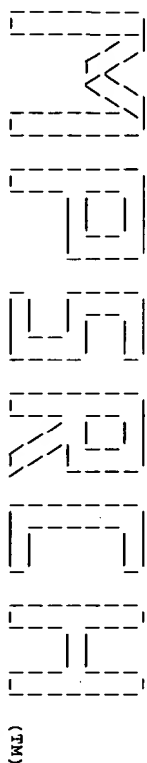
RESULT 8
 ID NOTC_XENLA STANDARD: PRT: 2524 AA.
 AC P21783;
 DT 01-MAY-1991 (REL. 18, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (NOTCH PROTEIN).
 GN NOTCH.
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX COFFMAN C., HARRIS W., KINTNER C.;
 RL SCIENCE 249:1438-1441(1990).
 RN [2]
 RP REVISIONS TO 1759-1782.
 RA KINTNER C.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBS DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.
 CC -1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIG/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
 DR EMBL: M3874; G1364263; -
 DR PIR: A35844; A35844.
 DR HSSP: P20693; 1ESL.
 DR PROSITE: P500010; ASX_HYDROXYL, 23.
 DR PROSITE: P501186; EGF_2, 29.
 DR PROSITE: P501187; EGF_CA, 21.
 KW DIFFERENTIATION; NEUROGENESIS; REPEAT; ANK REPEAT; EGF-LIKE DOMAIN; TRANSMEMBRANE; SIGNAL; GLYCOPROTEIN.
 FT SIGNAL 1 19
 FT CHAIN 20 2524
 FT DOMAIN 1729 1750
 FT DOMAIN 1751 2524
 FT DOMAIN 20 57
 FT DOMAIN 58 99
 FT DOMAIN 102 140
 FT DOMAIN 141 177
 FT DOMAIN 179 215
 FT DOMAIN 217 254
 FT DOMAIN 256 292
 FT DOMAIN 294 332
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 FT DOMAIN 371 409
 FT DOMAIN 411 449
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 FT DOMAIN 489 525
 FT DOMAIN 527 563
 FT DOMAIN 565 600
 FT DOMAIN 602 638
 FT DOMAIN 640 675
 FT DOMAIN 677 713
 FT DOMAIN 715 750
 FT DOMAIN 752 788
 FT DOMAIN 790 826
 FT DOMAIN 828 866
 FT DOMAIN 868 904
 FT DOMAIN 906 942

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FT DOMAIN 944 980 EGF-LIKE 25, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 982 1018 EGF-LIKE 26.
FT DOMAIN 1020 1056 EGF-LIKE 27, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1058 1094 EGF-LIKE 28.
FT DOMAIN 1096 1142 EGF-LIKE 29.
FT DOMAIN 1144 1180 EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1182 1218 EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1220 1264 EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1266 1304 EGF-LIKE 33.
FT DOMAIN 1306 1346 EGF-LIKE 34.
FT DOMAIN 1347 1383 EGF-LIKE 35.
FT DOMAIN 1386 1424 EGF-LIKE 36.
FT DOMAIN 1441 1560 3 X LIN/NOTCH REPEATS.
FT REPEAT 1441 1478 LIN/NOTCH 1.
FT REPEAT 1479 1520 LIN/NOTCH 2.
FT REPEAT 1521 1560 LIN/NOTCH 3.
FT DOMAIN 1871 2083 6 X ANK MOTIF REPEATS.
FT DISULFID 22 35 BY SIMILARITY.
FT DISULFID 29 45 BY SIMILARITY.
FT DISULFID 47 56 BY SIMILARITY.
FT DISULFID 62 74 BY SIMILARITY.
FT DISULFID 68 87 BY SIMILARITY.
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FT DISULFID 167 176 BY SIMILARITY.
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FT DISULFID 1390 1401 BY SIMILARITY.
FT DISULFID 1395 1412 BY SIMILARITY.
FT DISULFID 1414 1423 BY SIMILARITY.
FT CARBOHYD 462 462 POTENTIAL.
FT CARBOHYD 887 887 POTENTIAL.
FT CARBOHYD 958 958 POTENTIAL.
FT CARBOHYD 1178 1178 POTENTIAL.
FT CARBOHYD 1487 1487 POTENTIAL.
FT CARBOHYD 1508 1508 POTENTIAL.
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SQ SEQUENCE 2524 AA; 275123 MW; E63584B1 CRC32;

Query Match 5.28; Score 109; DB 1; Length 2524;
Best Local Similarity 16.08; Pred. No. 9,72e-05;
Matches 26; Conservative 18; Mismatches 109; Indels 10; Gaps 10;
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Db 1149 SPNPGCAGCTCTYLLGYSCECVAGHGVCSEINECLSHPCNGCTCIDLINTYKCA
QY 44 AAXXXCAEXXCSXXYTLR-QCYAGXX-NNXXXXXXAXEXLXXSSLVYV
Db 1209 PRG-TGVHC-EIN-VDDCPFDSTLEPKCINNKCIDRUG-YNCL-CEPGFVGEN
QY 102 KRGKKEKXKLXYWSXHXHXXGXHXXLESPEXP-VTSRLSDIFRXXSXXSXXDX
Db 1264 EGD-VNECLSNPCDSRGTONCLOLVNDYRCECROGFTGR-RCE 1304
QY 161 XXXKSNXCIDAAKACNLNDXCKKRLBSAYITXCKXXXSXKXERCN 203



(TM)

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Mpsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 13:08:00 1999; Maspar time 2460.88 Seconds
1236.356 Million cell updates/sec

Tabular output not generated.

Title: >US-08-866-354-41
Description: (1-1699) from US08866354.seq
Perfect Score: 1699
N.A. Sequence: 1 GCGCGCGCGTGCACGCGC.....CGACCGTGCAGCGCGCGCGC 1699
Comp: CGCGCGCGCGTGCACGCGC.....GTTGGCGTGCACGCGCGCGC

Scoring table: TABLE default
Gap 6

Mismatch STD : Dbase 0; Query 0

Searched: 2275026 segs, 895389244 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-est56
1:em-est1 2:em-gss1 3:em-gss2 4:em-gss3
Database: genbank-est109
5:gb-est1 6:gb-est10 7:gb-est11 8:gb-est12 9:gb-est13
10:gb-est14 11:gb-est15 12:gb-est16 13:gb-est17
14:gb-est18 15:gb-est19 16:gb-est2 17:gb-est20
18:gb-est21 19:gb-est23 20:gb-est24 21:gb-est25 22:gb-est26
23:gb-est27 24:gb-est28 25:gb-est29 26:gb-est31 27:gb-est32
28:gb-est33 29:gb-est34

Statistics: Mean 11.495; Variance 2.154; scale 5.337

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	381	22.4	442	22	AA049894 m11d08.r1 Soares	0.00e+00
2	349	20.5	465	21	m108d05.r1 Soares	0.00e+00
3	337	19.8	499	14	AA825330 UI-R-A1-ek-h-10-0-UI-S	0.00e+00
4	271	16.0	448	18	AA180186 EST223927 Normalized r	0.00e+00
5	254	14.9	353	21	AA041935 m104b08.r1 Soares	0.00e+00
6	251	14.8	431	18	AA179473 EST223187 Normalized r	0.00e+00
7	223	13.1	502	23	AA238748 m135d09.r1 Barstead	0.00e+00
8	128	7.5	387	20	m159f10.r1 Soares	0.00e+00
9	64	3.8	252	12	AA754459 97SN1787 Rice	5.49e-72
10	59	3.5	252	12	AA754459 97SN1787 Rice	1.56e-62
11	47	2.8	247	12	AA754458 97SN1784 Rice	1.26e-40
12	46	2.7	247	12	AA754458 97SN1784 Rice	7.20e-39
13	37	2.2	478	21	W73681 zds5h01.r1 Soares	1.11e-23

14	37	2.2	2275	11	AF034173	Homo sapiens ntcon2 co	1.11e-23
15	35	2.1	350	25	AA349976	EST56965 Infant brain	1.72e-20
16	36	2.1	2275	11	AF034173	Homo sapiens ntcon2 co	4.47e-22
17	30	1.8	205	17	AA783969	CG90781.f1 Aspergillus	6.60e-13
18	29	1.7	436	21	W69813	zds8906.r1 Soares	1.81e-11
19	29	1.7	792	18	AA035938	Mus musculus CDNA, c10	1.81e-11
20	27	1.6	374	23	AA144007	m175b01.r1 StrataGene	1.10e-08
21	27	1.6	409	23	AA153254	m175c01.r1 StrataGene	1.10e-08
22	28	1.6	436	21	W69813	zds8906.r1 Soares	1.81e-11
23	28	1.6	567	9	AA534427	ntf6d11.s1 NCI-CGAP	4.63e-10
24	27	1.6	667	12	AA0110816	Cit-HSP-2372014.TR CIT	1.10e-08
25	25	1.5	1287	12	AF038250	Homo sapiens clone ntc	4.63e-10
26	25	1.5	289	21	AA080800	Homo sapiens ntcon6 co	4.82e-06
27	25	1.5	360	13	AA809745	m299f10.s1 NCI-CGAP	4.82e-06
28	26	1.5	387	23	AA142537	m507804.r1 StrataGene	2.40e-07
29	25	1.5	394	29	AA014913	HS-3170.A1-G06-MR CIT	4.82e-06
30	26	1.5	415	13	AA839237	W958d06.r1 StrataGene	2.40e-07
31	25	1.5	421	16	R78049	y180a08.r1 Homo sapien	4.82e-07
32	25	1.5	430	20	W76716	m811h06.r1 Soares	4.82e-06
33	25	1.5	442	22	AA027705	ze33c03.s1 Soares	4.82e-06
34	25	1.5	446	6	AA587098	vc18b07.r1 KO mouse	4.82e-06
35	25	1.5	455	8	AA524878	ng46h10.s1 NCI-CGAP	4.82e-06
36	25	1.5	457	6	AA437089	z553a10.s1 Soares	4.82e-06
37	26	1.5	474	11	AA694259	z131d11.s1 Soares	2.40e-07
38	25	1.5	490	13	AA883883	Am6902.s1 Soares	4.82e-06
39	26	1.5	510	17	AT091539	OW59a01.x1 Soares	2.40e-07
40	26	1.5	521	7	AA530753	v144e07.r1 StrataGene	2.40e-07
41	25	1.5	566	27	FR0032477	Fugu rubripes GSS sequ	4.82e-06
42	26	1.5	631	7	AA518362	v110d02.r1 Barstead	2.40e-07
43	24	1.5	660	11	AF034177	Homo sapiens ntcon6 co	4.82e-06
44	24	1.4	445	7	RICS2438A	Rice CDNA, partial seq	8.83e-05
45	24	1.4	451	12	AA201294	LD042355.p1 Time LD Dros	8.83e-05

ALIGNMENTS

RESULT 1
LOCUS AA049894 442 bp mRNA EST 30-DEC-1996
DEFINITION m11d08.r1 Soares mouse embryo NBM13.5 14.5 Mus musculus CDNA
clone 475791 5', mRNA sequence.
AA049894
g1755226

KEYWORDS
SOURCE
ORGANISM

house mouse.
Mus musculus.
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

REFERENCE 1 (bases 1 to 442)

AUTHORS
Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Pridmore, G., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, P., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., et al.
The WashU-HMI Mouse EST Project
Unpublished (1996)
On Dec 31, 1996 this sequence version replaced g1:152956c.

TITLE
JOURNAL
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
W7:86535
Seq primer: -28M13 rev2 from Amerham
High quality sequence stop: 405.
Location/Qualifiers
1. 442
/organism="Mus musculus"

/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(47) primer [5'
TGTACCAATCTGATGAGTGGAGGCGGGAATTTTGTGTGTGTGT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
State Univ., from 2); double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="taxon:10090"
/clone="475791"
/clone_1lb="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
MUS
BASE COUNT
ORIGIN
79 a 142 c 122 g 99 t

Query Match 22.4%; Score 381; DB 22; Length 442;
Best Local Similarity 93.6%; Pred. No. 0.00e+00;
Matches 409; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 6 CTCGAATTTGCTATGCTGTGACTCTTACAGCAAGTGTGACCGCTGGCAGAGCCCTAC 65
|||||
544 CTCGAATTTGCTATGCTGTGACTCTTACAGCAAGTGTGACCGCTGGCAGAGCCCTAC 603
|||||
Db 66 GGGAGGAGCATGTCAGAGATCCGCTCGACGCGCACCCTGCTTACCCAGAGTGGCTCTC 125
|||||
Qy 604 GGGAGGAGCTGCTCAGAGATCCGCTCGACGCGCACCCTGCTTACCCAGAGTGGCTCTC 663
|||||
Db 126 TTTCTTTGAGAGGACAGAGTGTCCACGCTCAGAGGCTGTGCTGTGCTGTGCTGTGCA 185
|||||
Qy 664 TTTCTTTGAGAGGAGGACAGAGTGTCCACGCTCAGAGGCTGTGCTGTGCTGTGCTGTGCA 723
|||||
Db 186 GAAGATGCGGCGCTGTGAGGAGGCGGCGCTTAACACATGCCCCCAAGTTGGCCCTGCT 245
|||||
Qy 724 GAAGATGCGGCGCTGTGAGGAGGCGGCGCTTAACACATGCCCCCAAGTTGGCCCTGCT 783
|||||
Db 246 TCTGTAAACCCCAATTCCTGTGATCGGAGCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAG 305
|||||
Qy 784 TCTGTGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 843
|||||
Db 306 TCAGCGCTGATGAGCTTCAGACCCACATGTCATCTATGAGCATCTTGGGAGCTGTGCA 365
|||||
Qy 844 TCAGCGCTGATGAGCTTCAGACCCACATGTCATCTATGAGCATCTTGGGAGCTGTGCA 903
|||||
Db 366 ACTGAGCAGTCCAGATGTCTGCGGCGATACCTGGGCGATTTGGGAGCTGTGCA 425
|||||
Qy 904 ACTGAGCAGTCCAGATGTCTGCGGCGATACCTGGGCGATTTGGGAGCTGTGCA 963
|||||
Db 426 AACTTCATCAGCAAGT 442
|||||
Qy 964 AACTTCATCAGCAAGT 980
|||||

RESULT 2
LOCUS AA050083 465 bp mRNA EST 09-SEP-1996
DEFINITION m108d05.f1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone 475497 5', mRNA sequence.
ACCESSION AA050083
NID 91529753
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Mus.

REFERENCE 1 (bases 1 to 465)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubois,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, R.,
Schellenberg, R., Steptoe, M., Tan, F., Underwood, K., Moore, R.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
MGI:286241
High quality sequence stop: 431.
Location/Qualifiers
1..465
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(47) primer [5'
TGTACCAATCTGATGAGTGGAGGCGGGAATTTTGTGTGTGTGT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
State Univ., from 2); double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="taxon:10090"
/clone="475497"
/clone_1lb="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
MUS
BASE COUNT
ORIGIN
100 a 147 c 128 g 90 t

Query Match 20.5%; Score 349; DB 21; Length 465;
Best Local Similarity 90.4%; Pred. No. 0.00e+00;
Matches 424; Conservative 0; Mismatches 39; Indels 6; Gaps 5;

Db 3 CGGCGCCAGCG-AGCAGAGCGCTGTGCATCCGCGGCGCA--CCGCGCATGGGGCT 59
|||||
Qy 15 CGAGCGCCAGACAGAGAGCGTCCGCGGCTCCGCGCTCCAGACCCGCAATGGGGCT 74
|||||
Db 60 CTCTGAGGCC-GGAGCTCACTGTGATGATCTCTACTGCTGTGCTGTGCTGTGCTGTGCT 114
|||||
Qy 75 CTCCCGAGCGCGCGAGCGCGCGCGCTAGTATCTCTACTGCTGTGCTGTGCTGTGCTGTGCT 129
|||||
Db 119 GCCACTTGGAGCAGGAACCTCTTGCACAGAGACAGAGTTTGTGAACAGCTGTACTCT 154
|||||
Qy 135 ACCCTTGGAGCAGGAACCTCTTGCACAGAGACAGAGTTTGTGAACAGCTGTACTCT 169
|||||
Db 179 GGCAGAGAAATGAGAGCTAATCCGCTTGAAGGCGCTACAGACAGCTGAGCTG 204
|||||
Qy 195 GGCAGAGAAATGAGAGCTAATCCGCTTGAAGGCGCTACAGACAGCTGAGCTG 219
|||||
Db 239 CTGACCTTCAGT-TAAGAGCGCGCTCTAGAGAGTGTGCATGTCTGACAGCTG 254
|||||
Qy 255 CTGACCGCCAGCTGAGAGCTGACAGTCCCTCAGGGAGTGTGCCACATCTGCAGCGTG 319
|||||
Db 298 CCTAGAGGCA-CAGAACACTCAGAACAGCTCTGTGATGACTGAGGTGCCATCGGCG 356
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```

OY      315 CCTGTAAGCAGACAGCACTAGAGACAGCTCTCTCTATAGCTGACAGTCCACGCGC 374
Db      357 CATGAGACACCAAGCTACTCTGTGACATTATTGGACCTTACCTGCGCCAGAGCT 416
OY      375 CATGAGACACCAAGCTACTCTGTGACATTATTGGACCTTACCTGCGCCAGAGCT 434
Db      417 TGTGACTACGAGTTGATGTCTCACCCTATGAAGACAGACAGTACAGC 465
OY      435 TGTGACTACGAGTTGATGTCTCACCCTATGAAGACAGTACAGC 483

RESULT  3
LOCUS   AA925330 499 bp mRNA EST 21-APR-1998
DEFINITION  UR-R-A1-ek-h-10-0-UI-s1 UR-R-A1 Rattus norvegicus cDNA clone
            UR-R-A1-ek-h-10-0-UI-3 similar to g1126271591db|AB008833|AB008833
            Mus musculus mRNA for Gfra1pna-3, complete cds, mRNA sequence.
ACCESSION  AA925330
NID       G3072466
KEYWORDS  EST.
SOURCE    Norway rat.
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
          Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE  1 (bases 1 to 499)
          Bonaldo,M.F., Lennon,G. and Soares,M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
          97044477

JOURNAL  Program for Rat Gene Discovery and Mapping
MEDLINE  University of Iowa
          451 Eckstein Medical Research Building Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: mssoares@blue.weeg.iowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dT track (not shown) served to identify it as a clone from
the normalized adult kidney library. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
Seq primer: M13 forward.

FEATURES
Source
Location/Qualifiers
1..499
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/vector="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; The UR-R-A1
library is a subtracted library derived from the UR-R-A0
library. The UR-R-A0 library consisted of a mixture of
individually tagged normalized libraries constructed from
rat placenta, adult lung, brain, liver, kidney, heart,
spleen, ovary, and muscle. The tag is a string of 3-5
nucleotides present between the NotI site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-A1) was constructed as follows: PCR
amplified cDNA inserts from a pool of approximately 3,840
UR-R-A0 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UR-R-A0
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UR-R-A1 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"
/db_xref="taxon:10116"
/clone="UI-R-A1-ek-h-10-0-UI"
/clone_1lb="UI-R-A1"

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BASE COUNT 132 a 120 c 141 g 104 t 2 others
ORIGIN
Query Match 19.8%; Score 337; DB 14; Length 499;
Best Local Similarity 99.4%; Pred. No. 0.00e+00;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 161 GGTGGACACCAAGCTTCTCTCAAAAGGACCATTTTCTCAGCTGCTCAGAACCTTC 220
1685 GGTGGACACCAAGCTTCTCTCTCAAAAGGACCATTTTCTCAGCTGCTCAGAACCTTC 1526
Db 221 AGCTGCTCTCTCGAAGAACCAAGCAAGTATGAGTACATTCCTGGTGTCTC 2000
1685 GGTGGACACCAAGCTTCTCTCTCAAAAGGACCATTTTCTCAGCTGCTCAGAACCTTC 1526
CP 1625 AGCTGCTCTCTCGAAGAACCAAGCAAGTATGAGTACATTCCTGGTGTCTC 1526
Db 281 GGGAAACAGAGAGAGGCTGAGGTGGAGAGTAAATACACACCATATATACGCCANA 1526
1565 GGGAAACAGAGAGAGGCTGAGGTGGAGAGTAAATACACACCATATATACGCCANA 1526
CP 341 CTGAGATACAGAGTCTCTANGACAGACGCCAAGCAGAGTAAAGAGAGCTTTGA 1526
1505 CTGAGATACAGAGTCTCTANGACAGACGCCAAGCAGAGTAAAGAGAGCTTTGA 1526
Db 401 AGCTGGCGCTCAGATCTGAAGGCAAGCCCTGCTTCCAAAGCTCATCTG 450
1445 AGCTGGCGCTCAGATCTGAAGGCAAGCCCTGCTTCCAAAGCTCATCTG 1526
CP 461 AGCAGACAGATGTGACAGTGTGAGCTGTTGCATCTTCT 499
1385 AGCAGACAGATGTGACAGTGTGAGCTGTTGCATCTTCT 1347

RESULT 4
LOCUS A1180186 448 bp mRNA EST 08-07-1998
DEFINITION EST223927 Normalized rat spleen, Bento Soares Rattus sp. cDNA
            RSPCR62 3' end, mRNA sequence.
ACCESSION A1180186
NID       G3730824
KEYWORDS  EST.
SOURCE    Rattus sp.
ORGANISM  Rattus sp.
          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
          Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE  1 (bases 1 to 448)
          Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
          Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
          Gene Index
          Unpublished (1998)

JOURNAL  Contact: Lee, NH
MEDLINE  ATCC
          The Institute for Genomic Research
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.

FEATURES
Source
Location/Qualifiers
1..448
/organism="Rattus sp."
/strain="Organ: spleen; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
/db_xref="taxon:10118"
/clone="RSPCR62"
/clone_1lb="Normalized rat spleen, Bento Soares"
BASE COUNT 119 a 110 c 127 g 92 t
ORIGIN
Query Match 16.0%; Score 271; DB 18; Length 448;
Best Local Similarity 98.6%; Pred. No. 0.00e+00;

```


	BASE COUNT	114 a	102 c	123 g	91 t	1 others.
ORIGIN						
	Query Match	14.8%	Score 251:	DB 18;	Length 431:	
	Best Local Similarity	99.2%;	Pred. No. 0.00e+00;			
	Matches 253; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;	
Db	169 GGTGACCAAGCACCCTTCCTCCACAAGAAGGCACATTTTCTCATAGCGCTCCAGAACCTTC	228				
Cp	1685 GGTTGGACCAAGCACCCTTCCTCCACAAGAAGGCACATTTTCTCATAGCGCTCCAGAACCTTC	1626				
Db	229 AGCCTGCCCTTCCTGGAGAAAGCACCAAGGAATAGTAGACTCATTAAGCCTGGAGTGCTCT	288				
Cp	1675 AGCCTGCCCTTCCTGGAGAAAGCACCAAGGAATAGTAGACTCATTAAGCCTGGAGTGCTCT	1566				
Db	289 GGGAAAACAGGAAGAAGAGGCTGGAGGTGGGAGCTAATACCAACCAATAATACAGCCANA	348				
Cp	1565 GGGAAAACAGGAAGAAGAGGCTGGAGGTGGGAGCTAATACCAACCAATAATACAGCCANA	1506				
Db	349 CTGAGATTACAAAGTCTCTAGGAGGAGACAGCCCCAAGCAGAGATTAAGTACAGAGTTCAA	408				
Cp	1505 CTGAGATTACAAAGTCTCTAGGAGGAGACAGCCCCAAGCAGAGATTAAGTACAGAGTTCAA	1446				
Db	409 AGCTGGCCGCTCAG 422 					
Cp	1445 AGCTGGCCGCTCAG 1432 					
RESULT	7					
LOCUS	AA238748	502 bp	mRNA	EST	03-MAR-1997	
DEFINITION	mys5d09.r1 Barstead mouse pooled organs MFLB4 Mus musculus CDNA clone 697841 5', mRNA sequence.					
ACCESSION	AA238748					
NID	g1862771					
KEYWORDS	house mouse.					
SOURCE	Mus musculus					
ORGANISM	Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 502) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubugue,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepcewicz,W., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. Title The Mashu-HHMI Mouse EST Project Unpublished (1996)					
TITLE	The Mashu-HHMI Mouse EST Project					
JOURNAL COMMENT	Contact: Marra M/Mouse EST project WashU-HHMI Mouse EST project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mousee@watson.wustl.edu This clone is available royalty-free through INLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:431401 Seq primer: -28m13 rev2 ET from Amershams High quality sequence stop: 484. Location/Qualifiers 1..502 organism=Mus musculus" strain=FVB/N# note=vector: pRT7D-Pac (Pharmacia) with a modified polylinker Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAGTGGAGGAGCGCCGCCCTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [GTTGATTCGTAAC] digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. library constructed by Bob Barstead."					
FEATURES						
SOURCE						

/db_xref="taxon:10090"
 /clone="697841"
 /clone_id="Bartstead mouse pooled organs MPLRB4"
 /sex="mixed"
 /dev_stage="7 day"
 /lab_host="DH10B"
 <1. >502

MRNA
 BASE COUNT 94 a 157 c 122 g 129 t
 ORIGIN

Query Match 13.1%; Score 223; DB 23; Length 502;
 Best Local Similarity 88.3%; Pred. No. 0.006+00;
 Matches 257; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 15 TGAAGGCGCATGACAGCTAAGATGCGTTTCACACAGACGCTTCTCCAGAGACTGGCGAG 74
 |||||||
 Oy 1082 TGAAGGCGCATGCGGCTAAATGCGTTTCACACAGACACTCTTCTCCAGAGACTGGCGG 1141
 |||||||

Db 75 ACTCTACTTTTTCAGTGTGTGACAGACGAGAACAGAACCCCTGCTGTGAGACTGACGCCA 134
 |||||||
 Oy 1142 ACTCTACTTTTTCGTGTGATGAGACGACGACGAGAACAGACCCCTGCTGTGAGGCCACGCTCA 1201
 |||||||

Db 135 GGCATACCATCTTCTTCTTCATCATCTTCCCTGATTTCTGCTGACAGACCTCTGATAGC 194
 |||||||
 Oy 1202 GGCATACCATCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTGCTGATAGC 1261
 |||||||

Db 195 TGGGCTTCTCAGAGGCTCTTGTCTCTCCATCCACACACACACAGACAGATTTGACGCTGTGG 254
 |||||||
 Oy 1262 TGGGCTCCTCAGAGGCTCTTGTCT 1321
 |||||||

Db 255 TGGGAGAGAACTCGCCAGCCCTGTGGAGAGACGACGAGCTGTCTACACAGCA 305
 |||||||
 Oy 1322 TGGGAGAGAAATGCTGCTGCTCTGTGAAAGATGACACAGCCTCATCTGCA 1372
 |||||||

RESULT 8
 LOCUS W99197 387 bp mRNA EST 16-JUL-1996
 DEFINITION m595f10.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
 ACCESSION clone 418603 5', mRNA sequence.
 W99197
 MID g1429123
 SOURCE EST.
 ORGANISM house mouse.
 Mus musculus
 Vertebrate; Eutheria; Rodentia; Sclurognathl; Myomorpha; Muridae;
 Murinae; Mus.
 1 (bases 1 to 387)
 Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)

TITLE The WashU-HMI Mouse EST Project
 JOURNAL
 COMMENT
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63110
 Tel.: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL: confu-
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:25315
 Seq primer: ETPRimer
 High quality sequence stop: 341.
 Location/Qualifiers
 1..387
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified

strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTACCATCTGAGTGGAGCGGCCGATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Felima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W.

MRNA
BASE COUNT 112 a 145 c 130 g 90 t 1 others
ORIGIN
Query Match 15.1%; Score 335; DB 21; Length 478;
Best Local Similarity 88.5%; Pred. No. 0.00e+00;
Matches 418; Conservative 0; Mismatches 48; Indels 6; Gaps 6;

Db 1 TGACACTACTATGTGACTCCAGCCCGCATGCTGTCCTGTCAGAGCT 60
1585 TGACACCCCAACTATGTGACTCCAGCCCGCATGCTGTCCTGTCAGAGCT 1644
Db 61 GTCTGTGGACGGGAAACATGAGAGAGAGTGTGAGAAAGTTCCTCAGGACTTACCGAGA 120
1645 GTCTGTGGAGTGGAAACATGAGAGAGAGTGTGAGAAAGTTCCTCAGGACTTACCGAGA 1704
Db 121 ACCCATGCTCCGGGAAGCGCATCAGGCTTGN-AAGCGCAGGACGCTGAACTGCTCC 179
1705 ACCCATGCTCCGGGAAGCGCATCAGGCTTGN-AAGCGCAGGACGCTGAACTGCTCC 1764
Db 180 CAAAGGCCCCCTCTCTCCAGGCGCCAGGCGCC-TCGGGTGAGAGAGAGCGCTTTTGGC 238
1765 CAAAGGCCCCCTCTCTCCAGGCGCCAGGCGCC-TCGGGTGAGAGAGAGCGCTTTTGGC 1824
Db 233 CAGATGACTCTAGTACAGTACAGCTTGGGAGCAGATGTCTATCACCAGCTGTG 298
1825 CAGATGACTCTAGTACAGTACAGCTTGGGAGCAGATGTCTATCACCAGCTGTG 1884
Db 289 TCACGAGAGAGGGGCTGAGAGCGCAGCAACTCCAAAGATTAGATGTGCTTACAGAGC 358
1885 TCACGAGAGAGGGGCTGAGAGCGCAGCAACTCCAAAGATTAGATGTGCTTACAGAGC 1944
Db 359 TCACGAGCAAAATATCATCCAGGAGTAACAAGTATCAAACTTACCTACAGGCGCCAG 418
1945 TCAC-GACAAACATCATGTCAGGAGTAACAAAGTAT-CAAACTTACCTACAGGCGCCAG 2002
Db 419 CAGACGAGACCGGTGGCTTGGCTTGGACCTGCTGTGCTGATGATCTGA 470
2003 CAGACGAGACCGGTGGCTTGGCTTGGACCTGCTGTGCTGATGATCTGA 2052

RESULT 2
LOCUS AA349976 350 bp mRNA EST 21-APR-1997
DEFINITION EST56965 Infant brain Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA349976
NID g2002296
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 350)
AUTHORS Adams M.D., Kerlavage A.R., Fields C. and Venter J.C.
TITLE 3,400 expressed sequence tags identify diversity of transcripts from human brain
JOURNAL Nature Genet. 4, 256-267 (1993)

MEDLINE

93364420
COMMENT
Other-ESTs: THC102061
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hg1/hg1.html>)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
1..350
/organism="Homo sapiens"
/note="Organ: brain; Vector: lambda BD; Site: 1; HindIII; Site: 2; NotI."
/db_xref="AtCC (Inhost):150854"
/db_xref="taxon:9606"
/clone_1id="Infant brain"
/sex="female"
/dev_stage="Infant"

MRNA
BASE COUNT 80 a 105 c 93 g 62 t 10 others
ORIGIN

Query Match 12.0%; Score 266; DB 25; Length 350;
Best Local Similarity 87.2%; Pred. No. 0.00e+00;
Matches 306; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Db 1 CAGCCCCACTGGCATGCTGTGTCCTCCCTGTCAGCTGTCTGTGAGGCGGAACATGGA 60
1607 CAGCCCCACTGGCATGCTGTGTCCTCCCTGTCAGCTGTCTGTGAGGCGGAACATGGA 1666
Db 61 GGAGAGGTGAGAAAGTTCCTCAGGAGCTTACCGAGAACCATGCTCCGGAAGCCAT 120
1667 GGAGAGGTGAGAAAGTTCCTCAGGAGCTTACCGAGAACCATGCTCCGGAAGCCAT 1726
Db 121 CAGGCTTTGGCAAGCGCAGCAGTNAAGTNTCCCAAGGCGCCCTGTTCCAGCG 180
1727 CAGGCTTTGGCAAGCGCAGCAGTNAAGTNTCCCAAGGCGCCCTGTTCCAGCG 1786
Db 181 CACCCAGGCCCCCTCGGTGAGAGAGAGCGCTTTTCCAGATGACCTCAGTACAGTAC 240
1787 TACCCAGGCCCCCTCGGTGAGAGAGAGCGCTTTTCCAGATGACCTCAGTACAGTAC 1846
Db 241 CAGCTTGGGAGCAGTGTATCATCCAGCTGACGTTTTCAGAGAGAGGCGCTGAAGC 300
1847 CAGCTTGGGAGCAGTGTATCATCCAGCTGACGTTTTCAGAGAGAGGCGCTGAAGC 1906
Db 301 -AACCACTCCAAAGAGTTAAGCATGTNCTTACAGAGAGTCCAGCAAAATAT 350
1907 CAACAACCTCCAAAGAGTTAAGCATGTGCTTCCAGAGAGTCCAGCAAAACAT 1957

RESULT 3
LOCUS W73633 433 bp mRNA EST 16-OCT-1997
DEFINITION z655H01.s1 Soares fetal heart NBHL19W Homo sapiens cDNA
ACCESSION W73633
NID g1383767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS Hillier L., Clark N., Dubuque T., Ellington K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevisan E., Waterston R., Williamson A., Wohlmann P. and Wilson R.

DB	181	1318	7	416 bp	EST	21-APR-1997
DB	181	1318	7	416 bp	EST	21-APR-1997
LOCUS	AA350341	416 bp	MRNA	EST	21-APR-1997	
DEFINITION	EST57915	Infant brain	Homo sapiens	cDNA 5' end,	MRNA sequence.	
ACCESSION	AA350341					
NID	92002900					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Felder, R.A., White, O., Sutton, G., Blake, J.A., Brannon, R.C., Man, Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodde, J.A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.C., Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Seudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinko, D., Feng, D.-F., Ferrite, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, C., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, T.F., Wing, J., Xu, C., Yu, G., J., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.					
TITLE	Initial assessment of human genome diversity and expression patterns based upon 83 million nucleotides of cDNA sequence					
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)					
MEDLINE	96026280					
COMMENT	Other-ESTs: EST57914 THC102061 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/hgi/hgi.html) Seq primer: M13 Reverse.					
FEATURES	Location/Qualifiers					
source	1. 416 /organism="Homo sapiens" /note="Organ: brain; Vector: lambda B1; Site_1: HindIII; Site_2: NotI" /db_xref="ATCC (Inhost):151218" /db_xref="taxon:9606" /clone_1lb="Infant brain" /sex="female" /dev_stage="Infant" <1. >416					
BASE COUNT	116 a 116 c 93 g 86 t					
ORIGIN						
Query Match	8.6%; Score 190; DB 25; Length 416;					
Best Local Similarity	84.9%; Pred. No. 0.00e+00;					
Matches 241; Conservative	0; Mismatches 41; Indels 2; Gaps 2;					
DB	1	CCACCTGGCAGCTCTGTCTCCAGGAGCAGGAGGCTGTAAGCCCAACACTCAAAAGTTAAGC 60				
DB	1870	CCACCTGCG-ACACTCTATTCAGGAGCAGGAGGCTGTAAGCCCAACACTCAAAAGTTAAGC 1928				
DB	61	ATGTGCTTACAGAGCTCAAGCAACAATATCATCCAGGAGGATACAAAGGTGATCAAACT 120				

QY	1999	ATGTGCTTCACAGAGCTTCACAGACAAATATCATGTCACAGAGATATAAAAGTGATCAAACTT	1999
Db	121	AACTGAGCCCCACAGACAGCCAGCCGTGGCTGCTTGAACCGTGTGTCTGATG	1999
QY	1989	AACACAGGCTCACACAGACAGCCAGCTGTGGCTGCTTGAACCGCTCCACATGCTCAAT	1999
Db	181	CTGAACATCGGCTGTGTGAGCGCTGTGGGAACCGAGTCAAAATTTTGAAGCTATGATG	1999
QY	2049	CTGACCTTGGCGCTGTGTAGCGCTTTGGGAACCG -CACAAAAGTCTTCAAGCAACCCACA	1999
Db	241	CAGAACAGCCGCTGACGAAATGGAACACACACAGACACACA 284	1999
QY	2108	TATGATCATCCCGCTGACAAATGGAACACACACCATACACACA 2151	1999
RESULT	8		
LOCUS	H05619	418 bp	MRNA
DEFINITION	Y170a10.s1	Homo sapiens	CDNA clone 43207 3'
ACCESSION	H05619		
NID	9869171		
KEYWORDS	EST.		
SOURCE	human clone#43207 library-Soares	primate brain INIB vector-Lafmid	host-H10B (ampicillin resistant) primer-Promega -2ml3 Raitel-Mc
			I Raitel-2-Hind III Whole brain from a 73 days post natal female. 1
			strand cDNA was primed with a Not I - oligo(dT) primer [5',
			ACTGTGAAATATCCGCGCGCCGACAGAAATTTTCTTTTCTTTT 3']; double-strand
			cDNA was ligated to Hind III adaptors (Pharmacia), digested with
			Not I and directionally cloned into the Not I and Hind III sites
			the Lafmid BA vector. Library went through one round of
			normalization. Library constructed by Bento Soares and M. Fatima
			Bonaldi.
ORGANISM	Homo sapiens		
	Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;		
	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;		
	Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;		
	Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 418)		
AUTHORS	Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,		
	Holman,M., Huilman,M., Kucaba,T., Le,M., Lennon,G., Matira,M.,		
	Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F.,		
	Tveasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and		
	Wilson,R.		
TITLE	The Wash-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT			
	GDB: G00-415-748		
	Contact: Wilson RK		
	Washu-Merck EST Project		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@wustl.wustl.edu		
	High quality sequence stops: 364		
	Source: IMAGE Consortium, LBNL		
	This clone is available royalty-free through LBNL; contact the		
	IMAGE Consortium (info@image.lbnl.gov) for further information.		
FEATURES			
source	1..418		
	Location/Qualifiers		
	1..418		
	/organism="Homo sapiens"		
	/clone="43207"		
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ORIGIN			
Query Match	8.5%	Score 188;	DB 16; Length 418;
Best Local Similarity	83.0%;	Pred. No. 0.00e+00;	
Matches 312;	Conservative 0;	Mismatches 51;	Indels 13; Gaps 1
Db	43	TGTGCTGTGATGTTTCCATTTGTCAGAGCGCGCTGCTGTGCGCTANTTTTCAA	1999
QY	2151	TGTGTGATGCGTGTGTTTCATTTTGTGACGCGGAGTTCAATTCGTGGCTGTGAC	1999

CONTACT: Kerlavage, AR
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 The Institute for Genomic Research
 7112 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Hmdb: :
<http://www.tigr.org/tdb/hgl/hgl.html>
 Seq primer: M13 Reverse
 Location/Qualifiers
 1..225
 source

FEATURES	source	location/Qualifiers
BASE COUNT	119 a 184 c 157 g 74 t	32 others
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Query Match	5.7%	Score 149; DB 25; Length 225;
Best Local Similarity	85.4%	Pred. No. 1,62e-246;
Matches	187; Conservative	0; Mismatches 30; Indels 2; Gaps 2;
Db	3	TCGCTCTTCTTCTTCTTCTAGACGAGACCCCTCGCTCTTGTGGCAGACCCCTCTCCCTGC 62
Oy	691	TCCTCCCTCCCACTACCCAGACGAAACCTCCGCTCTTGTGGCAGACCCCTCTCCCTGC 750
Db	63	AGGGCCCCGAGCTCCACGCGCTGGCGCCCCAGTAGAGCTGTGC-GGGCCAAATNACTGT 121
Oy	751	AGGGCTCTGAGCTCCAGCGCTGGCGCCCCAGTAGAGCTGTGTGCGGCAATGAGCTGT 810
Db	122	GTGGCGCCGAATCCAACTGCAGCTCTGTGCACGNNACTCTGGCGCAGATGCTGTGGCAGNNC 181
Oy	811	GTGGCGCTGATCCCACTGCAGCTCCGATGACGACCACTCTGGCAGATGCTGTGGCAGNNC 870
Db	182	GGCAGCAACACCATCTGTGNC-AACAAGAGTTCACGG 219
Oy	871	GGGATCCCAATACCATCTGTGGCCAAATAGAGATGCCAGG 909
RESULT	11	
LOCUS	FR0032477	566 bp DNA GSS 27-JUN-1998
DEFINITION	Fugu rubripes GSS sequence, clone 142F04d9, genomic survey	
ACCESSION	AL028845	
NID	93270959	
KEYWORDS	GSS: genome survey sequence.	
SOURCE	Fugu rubripes.	
ORGANISM	Fugu rubripes.	
REFERENCE	1 (bases 1 to 566)	
AUTHORS	Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umranta, Y., Williams, G., and Brenner, S.	
TITLE	Direct Submission	
JOURNAL	Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email: biolhelphomp.mrc.ac.uk	
COMMENT	Vector: Bluescript II KS V_Type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.	
FEATURES		
source		
BASE COUNT	119 a 184 c 157 g 74 t	32 others
ORIGIN		
Query Match	5.2%	Score 116; DB 27; Length 566;
Best Local Similarity	66.8%	Pred. No. 2,50e-176;
Matches	217; Conservative	0; Mismatches 107; Indels 1; Gaps 1;
Db	26	CANCCGCGCCTGAGACGCCGCNAGCCTGCMACATGCAGCAGANNACTGCGAGAGCTCGG 85

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Db	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300
Db	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300
Db	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300
Db	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	12																																						

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BASE COUNT	154 a	174 c	166 g 133 t
ORIGIN			4 others

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Best Local Similarity	64.48;	Pred. No. 1.32e-159;		
Matches 319;	Conservative 0;	Mismatches 169;	Indels 7;	Gaps 5

Db	14	GTGCGCAAAAGCCCTCAGGAGAGTCTTTGCGCAAAAGTAACGACGCACACAGATACGGAT	73
Qy	1268	GTGCGCAAAAGGCTCTGGCCAGATCTTTTGAACCTGTGCCAGGAGATATACCTACCGCAT	1327
Db	74	GCTCTTTGCTCCTGCCGGAGCTGCCTGTACACGAGAGGCGGCGACAGACTATCGTCC	133
Qy	1328	GCCTCTTGTGCTCTGCTCAGGAGCACCAGCATGTGCTGTAGCTGCCTGCCGCAAAACATCTGCC	1387
Db	134	TGTGTGCTCCTATGAAGAAGCAGAGAGGCCCACTGCCGTGATCTGTGCAGAACTCCTGC	193
Qy	1388	CAGTGTCTCTTATGAGCAGCAGAGAGAACCCAACTGCTGTGACCTGTCCGACGCTGTGTGCG	1447
Db	194	GACAAATTTACATCTGCGAGATCTGCCCTTGACAGATTTTTTACCAACTGCCAGCCAGAT	253
Qy	1448	TACAGACCACTGTGCCGGTCCCGACCTGGGAGA-TTTCACGCCAACTGTGAGGCTCT	1506
Db	254	CAAGGTGTGCACCAACTGTCTTAAGSAGAACTACGACAACTGCTCCTGGCTTACTGG	313
Qy	1507	ACGGGCAATACCAAGCTGTCTGCCGGAACACTTACCAGGCAATGTGTGGGCTCTTATGCTG	1566
Db	314	GACTGATTTGCGACAGTCATGACTCTTACTACATAGACTCCAGCAGC-CT--CA--GTG-	367
Qy	1567	GCATGATTTGGGTTTGATATGACACCCCACTATGTGGATCCAAACCCCAAGGGCACTGTG	1626
Db	368	TGAGCGCGTGTGCTGCAATGTGCAGCAGCAGTGTGCGCAATGACCTGAGAAATTTGCTGAATTC	427
Qy	1627	TGCTCTCCCTGTGCAATTTGCTGGCGAGTGGGGAACATGGAAMAGAGTGTGAGAAATGCC	1686
Db	428	TGAATTTTTTAAAGGCAATAGCTGTCTTAAATAATGCAATTAAGCTTTTGGACATGGCT	487
Qy	1687	TCAGGAGCTTCAAGSAAAACCATGCTCTCCGAATGTCCATTCAGGCTTTTGTATATGCA	1746
Db	488	CGAGTGTGACCACT	502
Qy	1747	CAGATGTGAACATGT	1761

RESULT	13	EST	27-AUG-1998
LOCUS	A1003810	163 bp	RNA
DEFINITION	0f43c0l.g1 Soares_testis.NHT Homo sapiens cDNA clone IMAGE:16195220		
	3', similar to SM:NR1r-HUMAN 000451 NEURITRIN RECEPTOR ALPHA		
ACCESSION	PRECURSOR ; mRNA sequence.		
	A1003810		
NID	g3213320		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
REFERENCE	1 (bases 1 to 163)		
AUTHORS	Primates; Catarrhini; Homidae; Homo.		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/imagen/image.html

Trace considered overall poor quality
Insert Length: 1090 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
SOURCE

```

/organism="Homo sapiens"
/notice="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I -
primer [5]
TGTACCAATCTGAGTGGAGCGCCGCCCAATTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonafiglio."
/db_xref="taxon:9606"
/clone_name="IMAGE:1619530"
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/lab_host="DH10p"
29 a 51 c 33 g 30 t

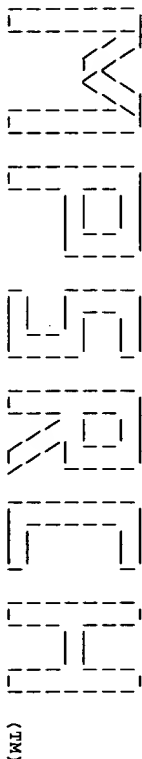
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Query Match	4.7%	Score 104	DB 17	Length 163
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Matches 132	Conservative 0	Mismatches 28	Indels 0	Gaps
DB	4	GCTCCGGACAGGCGGTGCAGGTGTGTATGACACTGTGTCCCAACCGGTACTGTGCATTA		
CP	1893	GCTCCTGTGATGTATGTGTGACAGGTGTGTATGACACTGTGTCCCAAGCTGTGTGTCTGATTA		
DB	64	GGTCATCTGGCAAGAAGGCGCTTCTCCACACAGGGCGCTGGTGTGGCCGGAACAA		
CP	1833	GGTCATCTGGCAGTAAAGAGATCTTCTCACCCGAGGGGCGCTGGGTAGTGGAGTCAAC		
DB	124	GGCCTTTGGACAGCTTTCACAGTTCAGTCCGTCGGTGGCCAAA	163	
CP	1773	GGCCTTTGGAGACATGTTTCACATCTGTGCCATTATCCAAA	1734	

RESULT	14
LOCUS	AA87098 446 bp mRNA EST 23-APR-1997
DEFINITION	vcl18B07.r1 KO mouse embryo 11 5dpc Mus musculus cDNA clone
ACCESSION	U01807
NID	AA87098
KEYWORDS	g2040052
SOURCE	EST.
ORGANISM	house mouse. Mus musculus. Eukaryotes; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Vertebrata.
REFERENCE	Martinez,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubnyche,I, 1 (bases 1 to 446) Gissel,S., Kueba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and Waterston,R.
AUTHORS	The Washn-HHMI Mouse EST Project Unpublished (1996)
TITLE	
JOURNAL	
COMMENT	

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

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MParch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Mar 11 18:15:43 1999; Maspar time 6064.12 Seconds
1249.739 Million cell updates/sec

Tabular output not generated.

Title: >US-08-866-354-35
Description: (1-4232) from US08866354.seq
Perfect Score: 4232
N.A. Sequence: 1 CATGAGAAACGTCAGTAG.....AAGGTCACATTAAGGTGGC 4232
Comp: GTCATCTTTGGAGTCATTC.....TTCGCGATTATTGCACGC

Scoring table: TABLE default
Gap 6

Match STD: Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-est56
1:em_estc1 2:em_gss1 3:em_gss2 4:em_gss3
Database: genbank-est109
5:gb_estc1 6:gb_estc10 7:gb_estc11 8:gb_estc12 9:gb_estc13
10:gb_estc14 11:gb_estc15 12:gb_estc16 13:gb_estc17
14:gb_estc18 15:gb_estc19 16:gb_estc2 17:gb_estc20
18:gb_estc21 19:gb_estc23 20:gb_estc24 21:gb_estc25 22:gb_estc26
23:gb_estc27 24:gb_estc28 25:gb_estc29 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 12.815; Variance 2.593; scale 4.942

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	426	10.1	478	21	W73681 zds5h01.r1 Soares feta	0.00e+00
2	403	9.5	476	13	AA747512 nx77d04.s1 NCI CGAP_Ew	0.00e+00
3	372	8.8	433	21	W73613 zds5h01.s1 Soares feta	0.00e+00
4	357	8.4	416	25	AA350341 ES57915 Infant brain	0.00e+00
5	352	8.3	364	5	R02135 yeb3h05.s1 Homo sapien	0.00e+00
6	345	8.2	353	19	HSC1KA112 H. sapiens partial CDN	0.00e+00
7	346	8.2	432	20	TS1669 Infant brain, B	0.00e+00
8	328	7.8	350	25	AA349976 ES57965 Infant brain	0.00e+00
9	312	7.4	418	15	H05619 y170a10.s1 Homo sapien	0.00e+00
10	307	7.3	317	20	HSC27A051 H. sapiens partial CDN	0.00e+00
11	307	7.3	321	25	H12961 y170a10.r1 Homo sapien	0.00e+00
12	294	6.9	304	16	AA350340 ES57914 Infant brain	0.00e+00
13	292	6.9	309	19	HSC1KA111 H. sapiens partial CDN	0.00e+00

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
14	288	6.8	319	23	T03342 IB189 Infant brain, B	0.00e+00
15	285	6.7	359	5	R00414 yel1f07.r1 Homo sapien	0.00e+00
16	239	5.6	247	14	AA866209 og98g12.s1 NCI CGAP_K1	0.00e+00
17	225	5.3	229	5	R02249 yeb3h05.r1 Homo sapien	0.00e+00
18	199	4.7	225	25	AA377675 ES70281 Synovial sarcoma	0.00e+00
19	170	4.0	390	14	AA848927 ES7191689 Normalized	0.00e+00
20	168	4.0	431	15	AI047785 uh83d10.r1 Soares feta	0.00e+00
21	139	3.3	163	17	AI003810 ct43c01.s1 Soares feta	0.00e+00
22	141	3.3	388	15	AI019799 ua93b10.r1 Soares feta	0.00e+00
23	138	3.3	424	21	AA48808 m43b10.r1 Soares feta	0.00e+00
24	128	3.0	566	27	FR0032477 Fugu rubripes GSS sequ	0.00e+00
25	124	2.9	283	18	AI137478 UI-R-C2p-ol-1-07-0-UI	0.00e+00
26	120	2.8	283	18	AI136025 ma01e02.r1 Soares feta	0.00e+00
27	115	2.7	314	9	W09562 UI-R-C2p-nx-C-02-0-UI	0.00e+00
28	102	2.4	631	7	AA518362 v110d02.r1 Soares feta	0.00e+00
29	94	2.2	446	6	AA387098 vcl8b07.r1 KO mouse em	0.00e+00
30	86	2.0	180	23	AA064450 m47h11.r1 StrataGene	0.00e+00
31	63	1.5	252	12	AA754459 97SN1787 Rice Immature	0.00e+00
32	64	1.5	428	24	AA271778 va72a08.r1 Soares feta	0.00e+00
33	60	1.4	252	12	AA754459 97SN1787 Rice Immature	0.00e+00
34	53	1.3	379	20	AA004055 mg81b07.r1 Soares feta	0.00e+00
35	53	1.3	382	26	FR0012298 F. rubripes GSS sequenc	0.00e+00
36	57	1.3	448	7	AA518754 V101f08.r1 Barstead mo	0.00e+00
37	55	1.3	523	14	AA848480 ES7191240 Normalized r	0.00e+00
38	53	1.3	569	27	FR0032480 Fugu rubripes GSS sequ	0.00e+00
39	53	1.3	577	21	AA008471 mg87a02.r1 Soares feta	0.00e+00
40	52	1.2	150	21	AA039187 m101h06.r1 Soares feta	0.00e+00
41	52	1.2	247	12	AA754458 97SN1787 Rice Immature	0.00e+00
42	52	1.2	294	16	R68056 yb9e11.r1 Homo sapien	0.00e+00
43	52	1.2	375	16	R73728 y155b03.r1 Homo sapien	0.00e+00
44	51	1.2	386	23	AA184518 mt50d04.r1 StrataGene	0.00e+00
45	52	1.2	495	8	AA549565 VK80d04.s1 Knowles Sol	0.00e+00

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	426	10.1	478	21	W73681 zds5h01.r1 Soares feta	0.00e+00
2	403	9.5	476	13	AA747512 nx77d04.s1 NCI CGAP_Ew	0.00e+00
3	372	8.8	433	21	W73613 zds5h01.s1 Soares feta	0.00e+00
4	357	8.4	416	25	AA350341 ES57915 Infant brain	0.00e+00
5	352	8.3	364	5	R02135 yeb3h05.s1 Homo sapien	0.00e+00
6	345	8.2	353	19	HSC1KA112 H. sapiens partial CDN	0.00e+00
7	346	8.2	432	20	TS1669 Infant brain, B	0.00e+00
8	328	7.8	350	25	AA349976 ES57965 Infant brain	0.00e+00
9	312	7.4	418	15	H05619 y170a10.s1 Homo sapien	0.00e+00
10	307	7.3	317	20	HSC27A051 H. sapiens partial CDN	0.00e+00
11	307	7.3	321	25	H12961 y170a10.r1 Homo sapien	0.00e+00
12	294	6.9	304	16	AA350340 ES57914 Infant brain	0.00e+00
13	292	6.9	309	19	HSC1KA111 H. sapiens partial CDN	0.00e+00

TITLE
JOURNAL
COMMENT

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63110

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LINT.

IMAGE Consortium (info@image.lint.gov) for further info.

Insert Length: 650 Std Error: 0.00

Seq primer: mob.REGA+ET

High quality sequence stop: 384.

FEATURES

Location/Qualifiers
1..478
/organism="Homo sapiens"
/note="Organ: heart; Vector: pT73D (Pharmacia) A
modified polylinker; Site_1: Not I; Site_2: Eco RI;

strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTGGAGCGGCCGACCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

/db_xref="taxon:9606"
/clone="344593"
/clone_lib="Soares fetal heart NbHL19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"

BASE COUNT 112 a 145 c 130 g 90 t 1 others
ORIGIN

Query Match 10.1% Score 426 DB 21 Length 478;
Best Local Similarity 98.1% Pred. No. 0.00e+00;
Matches 464; Conservative 0; Mismatches 3; Indels 6; Gaps 6;

Db 1 TGACACCTAATCTATGTGACTCCAGCCCATCTGCATCTGTCTCCCTGTGTACACT 60
Oy 2500 TGACACCTAATCTATGTGACTCCAGCCCATCTGCATCTGTCTCCCTGTGTACACT 2559
Db 61 GTCTGTGAGGCGGGAACATGAGAGAGAGTGTGAGAAATCTCTCAGGACCTTACCGAGA 120
Oy 2560 GTCTGTGAGGCGGGAACATGAGAGAGAGTGTGAGAAATCTCTCAGGACCTTACCGAGA 2619
Db 121 ACCCATGCTCTCGGAGAACCATCCAGGCTTTGN-AACGGCAGGAGCTGAACGTGTCC 179
Oy 2620 ACCCATGCTCTCGGAGAACCATCCAGGCTTTGN-AACGGCAGGAGCTGAACGTGTCC 2679
Db 180 CAAAAGGCCCTCGTTCAGAGGCCACCAAGGCC-TCGGGTGAGAGAGAGGCTTCTTTCG 238
Oy 2680 CAAAAGGCCCTCGTTCAGAGGCCACCAAGGCC-TCGGGTGAGAGAGAGGCTTCTTTCG 2739
Db 239 CAGATGACCTCAGTACAGTACAGTGTGGGAGCAGATGTATCATCCACCTGACAGTGTG 298
Oy 2740 CAGATGACCTCAGTACAGTACAGTGTGGGAGCAGATGTATCATCCACCTGACAGTGTG 2799
Db 299 TCAGAGCAGGAGGCTGAGAGGCAACACCTCAAGAGTAAAGTATGATTCACAGAGC 358
Oy 2800 TCAGAGCAGGAGGCTGAGAGGCAACACCTCAAGAGTAAAGTATGATTCACAGAGC 2859
Db 359 TCACGACAAATATCATCCAGGAGTAACAAGTATCAAACTTAACCTCAGGCCCCAG 418
Oy 2860 TCACGACAAATATCATCCAGGAGTAACAAGTATCAAACTTAACCTCAGGCCCCAG 2917
Db 419 CAGAGCAGAGCCTGTGCTGTGACCTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGT 471
Oy 2918 CAGAGCAGAGCCTGTGCTGTGACCTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGT 2968

RESULT 2 AA747512 476 bp mRNA EST 18-FEB-1998
LOCUS
DEFINITION nx77d04.s1 NCI-CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268263, mRNA
SEQUENCE
ACCESSION AA747512
NID 92787470
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 476)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Eiden, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/Link at: www-bio.11nl.gov/db/tp/image/image.html

Insert Length: 361 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence step: 401.
Location/Qualifiers

FEATURES

SOURCE

1. 476
/organism="Homo sapiens"
/note="Vector: PAMP10; mRNA made from Ewing's sarcoma cDNA made by oligo-dT priming. Non-directional."
Size-selected on agarose gel, average insert size: 56:5380-5383."
Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
/db_xref="taxon:9606"
/clone="IMAGE:1268263"
/clone_lib="NCI-CGAP_Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"

BASE COUNT 131 a 104 c 119 g 121 t 1 others
ORIGIN

Query Match 9.5% Score 403 DB 13 Length 476;
Best Local Similarity 97.3% Pred. No. 0.00e+00;
Matches 429; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

Db 37 ACGTTTATGAGAGCTTGTGTTAAGCTTGATGGGATCAGAGAGCCGCCACAGGCCAG 96
Cp 4229 ACGTTTATGAGAGCTTGTGTTAAGCTTGATGGGATCAGAGAGCCGCCACAGGCCAG 4170
Db 97 CCAAGCTGACTGGGCGAGGCGACATGCGGGCCATGCTTTTCCCATTAATAGACAC 156
Cp 4169 CCAAGCTGACTGGGCGAGGCGACATGCGGGCCATGCTTTTCCCATTAATAGACAC 4110
Db 157 AGATTAATAAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 216
Cp 4109 AGATTAATAAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4050
Db 217 TCATAGTTTGTGCTTAATAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 276
Cp 4049 TCATAGTTTGTGCTTAATAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 3990
Db 277 GGATGTAT 336
Cp 3989 GGATGTAT 3930
Db 337 CGCTAGGAATGAGAAAGAGCGCGCAAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 396
Cp 3929 CGCTAGGAATGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3872
Db 397 AAGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 455
Cp 3871 AAGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 455
Db 456 CCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476
Cp 3811 CCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3791

RESULT 3 W73633 433 bp mRNA EST 16-OCT-1998
LOCUS
DEFINITION z653h01.s1 Soares fetal heart NbHL19W Homo sapiens cDNA clone IMAGE:1268263, mRNA sequence.
SEQUENCE
ACCESSION W73633
NID 344593
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 433)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

ACCESSION	M73633
NID	91383767
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes: Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrate: Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 433) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Holtman, M., Kucaba, T., Le, M., Lennon, G., Merrit, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.
TITLE	The Mashu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Mashu-Merck EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 650 Std Error: 0.00 Seq primer: mob. REGA+ET High quality sequence stop: 343. Location/Qualifiers 1..433 /organism="Homo sapiens" /note="Organ: heart; Vector: p773D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCACTGTGAAGTGGAGAGCGGCCGACATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Felipe Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHH19W." /db_xref="taxon:9606" /clone="344593" /clone_11b="Soares fetal heart NBHH19W" /sex="unknown" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" complement(1..>433) 109 c 132 g 120 t
BASE COUNT	72 a 109 c 132 g 120 t
ORIGIN	mRNA
Query Match	8.8%; Score 372; DB 21; Length 433; Best Local Similarity 97.9%; Pred. No. 0.00e+00; Matches 411; Conservative 0; Mismatches 3; Indels 6; Gaps 5;
Db	1 GCAAGGTGNTGTGTGCTGTGCTGCTGCTTCATTTGTCAGGCGGCTGCTGTGCGG 60
Cp	3077 GCAAGGTGTGTGTGTGTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGG 3018
Db	61 TA-CTTCAAAATCTTGTGACTCGGTTCCACAGGCTTCAAGGCTGTTTCAGATCAG 119
Cp	3017 TAGCTTCAAAATCTTGTGACTCGGTTCCACAGGCTTCAAGGCTGTTTCAGATCAG 2958
Db	120 GACACACGACGCGTCAAGGACGCGGCTGTGCTGTGCTGTGCGGCTGTGAGTTT 179
Cp	2957 GACACACGACGCGTCAAGGACGCGGCTGTGCTGTGCTGTGCGGCTGTGAGTTT 2898
Db	180 GATCACCTGTGTACCTCCCGGAGATATATTTGTCGTGACCTGTGTAAACACATGCTTAA 239
Cp	2897 GATCACCTGTGTACCTCCCGGAGATATATTTGTCGTGACCTGTGTAAACACATGCTTAA 2838

Db	240	CTTTTGAGAGTGTGTGGCTTCACCCCTGCTCTGGACAGAGTCGAGTGCATGAC	299
Cp	2837	CTCTTGAGAGTGTGTGGCTTCACCCCTGCTCTGGACAGAGTCGAGTGCATGAC	2778
Db	300	ACTGGGTCCCAAGCTGTACTGTCTACGTAGAGTCATCTGCGAAGAAGAGCGCTCTTCGA	359
Cp	2777	ACTGGT-TCGCCAGGTGTACTGTCTACGTAGAGTCATCTGCGAAGAAGAGCGCTCTTCGA	2719
Db	360	CCCGAGGGGCGCTGGGGTGGCTGGAGACGAGGGGCGCTTTTGGGGACACGTTACGTC	419
Cp	2718	CCCGAGGGGCGCTGGG-TGGCCTGGAGACGAGGGG-CCTTTT--GGGACACCTCTACGCTTC	2663
RESULT	4		
LOCUS	AA50341	416 bp	mRNA
DEFINITION	EST57915	Infant brain Homo sapiens	CDNA 5' end, mRNA sequence.
ACCESSION	AA50341		
NID	92002900		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.		
REFERENCE	1 (bases 1 to 416)		
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirsch,E.F., Weinstock,K.G., Gonsky,R., White,O., Sutton,G., Blake,J.A., Brandon,R.C., McInerney,J.O., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,E., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geach,J., Glodet,A., Gnehm,C.L., Hanna,M.C., Hedlom,E., Hunkler,C., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.K., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Phillips,C.A., Ryder,S.E., Scott,J.U., Sauder,D.M., Small,K.V., Spriggs,T.A., Uterback,M.R., Weidman,J.L., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,D., Dinko,D., Feng,D.-F., Ferrie,A., Fischer,C., Haslinger,A., He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kozak,D.L., Kunsch,C., HungJun,J., Li,H., Meltsner,P., Raymond,L., Wel,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fraser,C.M., and Venter,J.C.		
JOURNAL MEDLINE	Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)		
COMMENT	96026280 Other_ESTs: EST57914 THC102061 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: akkerlavet@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Index (http://www.tigr.org/tcbl/ngl/ngl.html) Seq primer: M13 Reverse.		
FEATURES	Location/Qualifiers		
SOURCE	1. 416		
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	/note="Organ: brain; Vector: lambda ID: Site_1: HindIII; Site_2: NotI"		
	/db_xref="ATCC (lnhost):151218"		
	/db_xref="taxon:9606"		
	/clone_lib="Infant brain"		
	/sex="female"		
	/dev_stage="Infant"		
	<1. 416		
ORIGIN	116 a 116 c 93 g 86 t 5 others		

RESULT	8	AA349976	350 bp	MRNA	EST	21-APR-1997
LOCUS		AA349976	350 bp	MRNA	EST	21-APR-1997
DEFINITION		EST55965	Infant brain	Homo sapiens	cDNA 5' end, mRNA sequence.	
ACCESSION		AA349976				
NID		q2002296				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		1 (bases 1 to 350)				
AUTHORS		Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.				
TITLE		3,400 expressed sequence tags identify diversity of transcripts from human brain				
JOURNAL		Nature Genet. 4, 256-267 (1993)				
MEDLINE		93364420				
COMMENT		Other ESTs: THC102061 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlavage@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse. Location/Qualifiers 1..350 /organism="Homo sapiens" /note="Organ: brain; Vector: lambda1d BA; Site_1: HindIII; Site_2: NotI" /db_xref="ATCC (inhost):150854" /db_xref="taxon:9606" /clone_lib="infant brain" /sex="female" /dev_stage="infant" <1..350 80 a 105 c 93 g 62 t 10 others				
BASE COUNT		80 a 105 c 93 g 62 t 10 others				
ORIGIN		MRNA				
		Query Match 7.8%; Score 328; DB 25; Length 350; Best Local Similarity 96.0%; Prid. No. 0.00e+00; Matches 337; Conservative 0; Mismatches 13; Indels 1; Caps 1;				
		1 CAGCCCCACATGCGATCTGCTGTCTCCCTCGTGACGTGTCTGTGNNAGCGGGAACATGGA 60				
		2522 CAGCCCCACATGCGATCTGCTGTCTCCCTCGTGACGTGTCTGTGNNAGCGGGAACATGGA 2581				
		61 GGAGAGAGTGNAGAAAGTTCCTCAGAGGACTCACCAGAGAACCCATGCTCCGGAAGCGCAT 120				
		2582 GGAGAGAGTGNAGAAAGTTCCTCAGAGGACTCACCAGAGAACCCATGCTCCGGAAGCGCAT 2641				
		121 CCAAGCCTTTGGCAACGCGACGACGAGTNAAGTNTCCCAAAAGGCCCCCTCTCCAGGC 180				
		2642 CCAAGCCTTTGGCAACGCGACGACGAGTNAAGTNTCCCAAAAGGCCCCCTCTCCAGGC 2701				
		181 CACCCAGGCCCCCTCGGNTGGAGAGACGCTCTTTTCCAGATGACTCATGTTNACAGTAC 240				
		2702 CACCCAGGCCCCCTCGGNTGGAGAGACGCTCTTTTCCAGATGACTCATGTTNACAGTAC 2761				
		241 CAGCTTGGGAGCAGATGTCATCACACCTGACGATTTNTCCAGAGAGCAGGGGCTGAAGG 300				
		2762 CAGCTTGGGAGCAGATGTCATCACACCTGACGATTTNTCCAGAGAGCAGGGGCTGAAGG 2821				
		301 -AACCACTCCAAAGAGTTAAGCATGTGTTCTTACAGAGCTCAGCGCAATAT 350				
		2822 CAACAAGTCCAAAGAGTTAAGCATGTGTTCTTACAGAGCTCAGCGCAATAT 2872				

LOCUS	H05619	418 bp	mRNA	EST	21-JUN-1995
DEFINITION	Y170a10.s1 Homo sapiens cDNA clone 43207 3'.				
ACCESSION	H05619				
NID	9869171				
KEYWORDS	EST.				
SOURCE	human clone=43207 library=Soares infant brain INIB vector=Lafmid 1A host=PHOB (ampicillin resistant, primer=Promega -22ml3 RstE1-NciI, I RstE2-Hind III whole brain from a 73 days post natal female, 1st, strand cDNA was primed with a Not I - Oligo(dt) primer (5' AACTGGAAATATTCGGCGCCGAGCAATTTTATTTTATTTT 3'); double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Felima Bonaldi.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 418)				
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucab, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.				
TITLE	The WashU-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	GDB: 600-415-748 Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 364 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN. Contact: IMAGE Consortium (info@image.lnl.gov) for further information. Location/Qualifiers 1. 418 /organism="Homo sapiens" /clone="43207"				
BASE COUNT	73 a	94 c	116 g	127 t	8 others
ORIGIN					
Query Match	7.4%; Score 312; DB 16; Length 418;				
Best Local Similarity	95.1%; Pred. NO. 0.00e+00;				
Matches	388; Conservative 0; Mismatches 8; Indels 12; Gaps				
Db	11	TTGGAAAAACAATTTTTTTTTTTCGAAGGTGCTGTGTCTCTGTGTGTTTCCATTTC	7		
Cp	3099	TGGGAAAAACAATTTTTTTTTTTCGAAGGTGCTGTGTGTGTGTGTTTCCATTTC	71		
Db	71	CAGGCGGTGTTCTTGTCTGCGTANTTTCAAAATCTTCTGACGCGTCCCAACATC	29		
Cp	3039	CAGGCGGTGTTCTTGTCTGCGTANTTTCAAAATCTTCTGACGCGTCCCAACATC	1		
Db	131	ACAAGGCTGTTTACGATCAGACAGACAGACAGCGTCAGAGCCGACGATCAGATC	10		
Cp	2979	ACAAGGCCAGTTTTCAGCATCAGACAGACAGACAGCGTCAGAGCCGACGATCAGATC	1		
Db	191	TGCTGGGGCCGAGTTAGTTTGATGATCACTCTTACTTCCTCTGGGATGATATTNTGCTA	24		
Cp	2919	TGCTGGGGCCGAGTTAGTTTGATGATCACTCTTACTTCCTCTGGGATGATATTNTGCTA	24		
Db	251	GCTGTGTAACACATGTTAACTCTTTGAGTTNTTGGCCTTCAGCCCGCTCTGGG	310		
Cp	2859	GCTGTGTAACACATGTTAACTCTTTGAGTTNTTGGCCTTCAGCCCGCTCTGGG	24		
Db	311	ACAGAACCTGCAGAGTGGGTGATGACACTGGGCCCCAAGGCTGGTACTGTCACTGAGG	310		

CP	2800	ACAGA-CGGGAGG-TGG-TGATGACACTGG-TCCCAAG-CTGG-TACTGTACTGAGG	2747
DB	371	GTCACTCTGNCMAAGNAGNGCTTTTCTCCACCCGAGGGCCGGG	418
CP	2746	-TCATCTGG-CAAG-AGG-CGCTCT-CTCCACCAGGGGCGCTGGG	2704
RESULT	10		
LOCUS	HSC2YA051	317 bp	RNA
DEFINITION	H. sapiens partial cDNA sequence: clone c-2ya05, mRNA sequence.		
ACCESSION	F08597		
NID	9677164		
KEYWORDS	EST; partial cDNA sequence; transcribed sequence fragment.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 317)		
TITLE	Genexpress.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (11-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 91801 Villejuif Cedex France E-mail: genexpress@genethon.fr		
AUTHORS	2 (bases 1 to 317)		
TITLE	Genexpress.		
JOURNAL	The Genexpress cDNA program		
REFERENCE	Unpublished		
AUTHORS	3 (bases 1 to 317)		
TITLE	Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houllatte,R., Juneau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Marlage-Sanson,R., Pietu,G., Pouillot,Y., Sebastien-Kabackis,C. and Tessier,A.		
JOURNAL	IMAGE: molecular integration of the analysis of the human genome and its expression		
REFERENCE	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)		
AUTHORS	95277534		
TITLE	Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3', into the HindIII -> NotI sites of the lambda BA vector.		
JOURNAL	Sequencing method: single read, full automatic;		
REFERENCE	Primer: M13 reverse		
AUTHORS	cDNA sequence colinear to mRNA		
TITLE	Stretch removed: nothing		
JOURNAL	Normalization method: Bento Soares, P.N.A.S. 91:9228-9232(1994);		
REFERENCE	Genexpress library_idt: C;		
AUTHORS	Genexpress sequence_idt: Y1C-2ya05.		
TITLE	Location/Qualifiers		
JOURNAL	1. 317		
REFERENCE	/organism="Homo sapiens"		
AUTHORS	/isolate="muscular atrophy patient"		
TITLE	/db_xref="taxon:9606"		
JOURNAL	/clone_lib="normalized infant brain cDNA from B.Souares, psychiatry Dept. Columbia University USA"		
REFERENCE	/sex="female"		
AUTHORS	/tissue_type="total brain"		
TITLE	/dev_stage="3 months old"		
JOURNAL	/dev_stage="3 months old"		
REFERENCE	BASE COUNT	47 a	84 c
AUTHORS	87 g	89 t	10 others
TITLE	ORIGIN		
JOURNAL	Query Match	7.3%	Score 307; DB 20; Length 317;
REFERENCE	Best Local Similarity	96.8%	Pred. No. 0.00e+00;
AUTHORS	Matches 307; Conservative	0;	Mismatches 10; Indels 0; Gaps 0;
TITLE	DB	1	GGCTGGGGGCGGACGCTCCAGAGGGGCTTGAGAGCTGAGCTGCGTGGNAGCCCTTNGG
JOURNAL	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
REFERENCE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
AUTHORS	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
TITLE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
JOURNAL	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
REFERENCE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
AUTHORS	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
TITLE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
JOURNAL	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
REFERENCE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
AUTHORS	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
TITLE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
JOURNAL	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
REFERENCE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
AUTHORS	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
TITLE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
JOURNAL	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
REFERENCE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
AUTHORS	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
TITLE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
JOURNAL	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
REFERENCE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
AUTHORS	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
TITLE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
JOURNAL	61	CGAGGCACTTAAACTTGGGACACAGCTTCTTNTCGGTGCGAGAAATTTNAAGTCAGAG	120
REFERENCE	61	CGAGGCACTTAAACTTGGGACACAGCTTCTT	

QY	3748	AAAAAGGAGCTTTGTTGGCTCTTTCGTTTCGTTGGGTCCTTTGGAGGCGTCCCTT	3807
Db	181	GGGAGAGAGGAGGAGAGACACACAGCCGGGTGTGTCTGCAGCAGCAGTGGGCGCTCA	240
QY	3808	GGGAGAGAGGAGGAGAGACACACAGCCGGGTGTGTCTGCAGCAGCAGTGGGCGCTCA	3867
Db	241	GCTTCGTCGTGTTTTCCTCCCGTCGTCCTTTCCTTTCCTTTCCTTCATTCCTTGA	300
QY	3868	GCTTCGTCGTGTTTTCCTCCCGTCGTCCTTTCCTTTCCTTTCCTTCATTCCTTGA	3927
Db	301	CGTACGTCACTGTATG	317
QY	3928	CGTACGTCACTGTATG	3944
RESULT	11		
LOCUS	H12981	521 bp	mRNA
DEFINITION	X170a10.r1 Homo sapiens cDNA clone 43207 5'.		
ACCESSION	H12981		
NID	9877801		
KEYWORDS	EST.		
SOURCE	human clone=43207 library=Soares infant brain INTB vector=lambda host=PHID (ampicillin resistant) primer=M13R1 SalI=Not I SalI=Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' ACTGCAAGCATTCGCGCCGACGAAATTTTATTTTATTTT 3'; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the lambdaid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bernaldo.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 521) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marre,M., Parsons,T., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.		
TITLE	The Washu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	GDB: G00-415-748 Contact: Wilson RK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63107 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence stops: 278 Source: IMAGE Consortium, LNLN This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers 1..521 /organism="Homo sapiens" /clone="43207"		
BASE COUNT	95 a	154 c	144 g
ORIGIN	119 t	9 others	
Query Match	7.3%	Score 307;	DB 16; Length 521;
Best Local Similarity	93.6%;	Pred. No. 0.0de+00;	
Matches 396;	Conservative	0;	Mismatches 14; Indels 13; Gaps
Db	1	CAACCATTCGCTGGAGATCGTCGCAAGGCGCTGACACCTGAATGACACATGCAAGAAGCTTC	
QY	2060	CAACCATTCGCTGGAGATCGTCGCAAGGCGCTGACACCTGAATGACACATGCAAGAAGCTTC	

Db	61	GCCTCTCATATCCTCATCTGCAACCGGAGATCTCGCCACACGAGCGCTGCACACGCC	120
Qy	2119	GCTCTCTCATATCTCATCTGCAACCGGAGATCTCGCCACACGAGCGCTGCACACGCC	2178
Db	121	GCAAGTGCACAAAGGCCCTCGCCAGTCTTCTTACCCGGGGTGGCCAGCAGTACACTACC	180
Qy	2179	GCAAGTGCACAAAGGCCCTCGCCAGTCTTCTTACCCGGGGTGGCCAGCAGTACACTACC	2238
Db	181	GCATGCTCTTCTGCTCCTGCCAAAGACAGGCGGTGCGCTTAGCCCGGGMCA-AAACCATCC	239
Qy	2239	GCAATGCTCTTCTGCTCCTGCCAAAGACAGGCGGTGCGCTTAGCCCGGGCAAAACATCC	2298
Db	240	TGCCCCACTGCTCTATGAGAGAAAGAGAGCCCAATGCGCTGGAGACTGCTGTGGCTG	299
Qy	2299	TGCCCACTGCTCTATGAGAGAAAGAGAGCCCAATGCGCTGG-ACCTGCTGTGGCTG	2357
Db	300	TGCCGGACTGACCACTCTGTGTGCGTCCGCGCTGAGCCACATCTTCATGAGCCAAATTGTT	359
Qy	2358	TGGCGG-ACGTGACCACTGTGTGTGTCCGGCT-GGCGCACTT-CCATG-CCAAATT-GTC	2412
Db	360	GGAGCCCTTCCATCCACAGCGGGGTGANCAGGTGCTTGGCGACAAATTACACAGGGTNTTT	419
Qy	2413	G-AGCCT-CCATCCAGACGG-TCCACAGCT-GCCCTGCGGACAAATT-ACCAGGCGCTGTCT	2467
Db	420	TGG 422	
Qy	2468	GCG 2470	

RESULT	12	304 bp	mrna	EST	21-APR-1997
LOCUS	AA350340				
DEFINITION	EST575914	Infant brain	Homo sapiens	CDNA, mRNA	sequence.
ACCESSION	AA350340				
NID	92002899				

SOURCE
ORGANISM

REFERENCE	AUTHORS	TITLE
1 (pages 1 to 304)	Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.	3,400 expressed sequence tags identify diversity of transcripts from human brain

**MEDLINE
COMMENT**

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel.: 3018699056
Fax: 3018699423
Email: arkerave@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>).

FEATURES

1. .304.

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/organism="Homo sapiens"
/note="Organ: brain; Vector: lafm1d BA; Site_1: HindIII;

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2
 3
 4

6

STAINING 9 7 96

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Best Local Similarity 97.08; Pred. NO. 0.00e+00;
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Db	1	CGCTCATCTGTTGGGGTATTATTTCATAGTTTGTTCCTTAAAAAAGAAAGAAAGG							
Cp	4072	CGCTCATCTGTTGGGGTATTATTTCATAGTTTGTTCCTTAAAAAAGAAAGAAAGG							
Db	61	GAAAACCAACAATATATGTATATGATGTGTATACATATATGTGTGAGACGACG							
Cp	4012	GAAAACCAACAATATATGTATATGATGTGTATACATATATGTGTGAGACGACG							
Db	121	GGTATGACATACAGTTGACGTACGNTGGAATNAGAAAGAAAGAAAGGAGAT							
Cp	3952	GGTATGACATACAGTTGACGTACGNTGGAATNAGAAAGAAAGAAAGGAGAT							
Db	181	AGGAGAGAAGACAGACAGAAAGCTTGAGGGCCACGCTGTCAGACACACAC							
Cp	3892	AGGAGAGAAGACAGACAGAAAGCTTGAGGGCCACGCTGTCAGACACACAC							
Db	241	TGTGCTTCTCCCTCCCTTNTCCCAAGGAGAGGCTTCGCAAAAGACCCACGAAAGA							
Cp	3832	TGTGCTTCTCCCTCCCTTNTCCCAAGGAGAGGCTTCGCAAAAGACCCACGAAAGA							
Db	301	AAGA							
Cp	3772	AAGA							

LOCUS	RESULT	13
LOCUS	HSC1KAI1	309 bp
DEFINITION	H. sepiens partial CDNA sequence; clone C-1kai1, mRNA	21-5'
ACCESSION	243761	
NID	9571865	
KEYWORDS	EST; partial CDNA sequence; transcribed sequence	180000
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE

TITLE
JOURNAL

and Genetique Molculaire et Biologie du developpement, CNRS UPR414,
B.P. 8, 94801 Villejuif Cedex France. E-mail: genexpress@genethon.fr
2 (bases 1 to 309)
REFERENCE
Genexpress.
AUTHORS

JOURNAL REFERENCE

TITLE

JOURNAL

COMMENT

Clonidine Library from B. Soares, Psychiatry Dept. Columbia University
USA;

Cloning_method: total mRNA was oligo-(dT) primed and directionall

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vector;
cout<<endl;
return 0;
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Primer: M13_reverse
cDNA sequence colinear to mRNA

Normalization method: Bento Soares, P.N.A.S in press

Genexpress_sequence_idt: y1c-1ka11;

No significant homology found with :
 genbank release 81 swissprot release 28
 location/Qualifiers

FEATURES

Source

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source
1..309
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/isolate="muscular atrophy patient"
/db_xref="taxon:9606"
/dev_stage="3 months old"
/tissue_type="total brain"
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/sex="Female"

BASE COUNT      80 a      81 c      79 g      67 t      2 others
ORIGIN

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Query Match	6.98;	Score 292;	DB 19;	Length 309;
Post Local Start/End	67.78;	Prod No 0	000+00.	

[illegible]

RESULT	14
LOCUS	T03342 319 bp MNNA EST 14-FEB-1997
DEFINITION	I81289 Infant brain, Bento Soares Homo sapiens CDNA clone I81289 3'end, mRNA sequence.
ACCESSION	T03342
NID	9314582
KEYWORDS	EST.
SOURCE	human. <i>Homo sapiens</i>
ORGANISM	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 319)
REFERENCE	Rhan,A.S., Wilcox,A.S., Polymeropoulos,M.H., Hopkins,J.A., Stevens,T.J., Robinson,M., Orpana,A.K. and Sikela,J.M. Single pass sequencing and physical and genetic mapping of human CDMS
TITLE	Nature Genet. 2, 180-185 (1992)
JOURNAL MEDLINE	94258200
COMMENT	On Jul 31, 1993 this sequence version replaced g1:275999.

Soares, Columbia University, was oligo-(dT) primed using directionally cloned into an M13-derived plasmid using total brain mRNA from a 72-day old human female affixed with spinal muscular atrophy."

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/db_xref="taxon:9606"
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complement("<1..>319")
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gene

mRNA

BASE COUNT

ORIGIN

60 a 73 c 87 g 92 t 7 other:s

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Best Local Similarity 94.7%; Pred. No. 0.00e+00;
Matches 303; Conservative 0; Mismatches 16; Indels 0;
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Cp	3098	GGGAAAACAAATTTTTTTTTTGCAGGTGTGTGTGTGTGTGTGTTCATTTGCTT	
Dd	61	AGCGGGCTGTCCITTTGTCTGGTAG-TTCAAATAATTTTGACTGGTTCCACAGCCTTA	
Cp	3038	AGGGGGGTGTTCTGTCTGTCTGTGGTAGCTTTAAAAAATTTTGTGACTGGTTCACAGGCCAA	
Dd	120	CAAGGCTGTATTAAGCATCTAGSACACACAGACGGTCAAGGAGCGACGGTCTGCTCT	
Cp	2978	CAAGGCCAATTTTCAGCATCTAGGACACACACACACACGGTCAAGGAGCGAGGCTCTGA	
Dd	180	GCTGGGGCCTGAGTAGAGTTTNCACCCTGTGAACCTCCCTGGGATGATATTTGCTGAGT	
Cp	2918	GCTGGGGCCTGAGTAGTAGTTGATTCACCTGTACTCCCTGGGATGATATTTGCTGAGT	
Dd	240	CNCTGTANAGCATGTTTAACTCTTTGGAGTTNTGGCTTCAGCCCCCTGCCCCTGAGC	
Cp	2858	CTCTGTAAACACAACTGGTTAACTTTTGGAGTTGTGTGGCCTTCAGCCCCCTGCTCTCGAG	
Dd	300	AGACGTGACAGTGGTGATGA 319	
Cp	2798	AGACGTGACAGTGGTGATGA 2779	

LOCUS	RESULT	15	359 bp	mRNA	EST	31-MAR-1995
DEFINITION	ye71f07.r1	Homo sapiens	CDNA clone	123205	5'	
ACCESSION	R00414					
KEYWORDS	9750150					
EST.	human clone-123205	library=Saare	fetal liver	spleen	INFUS	
SOURCE						

RESULT	15					
LOCUS	R00414	359 bp	mRNA	EST		31-MAR-1995
DEFINITION	ye11107.r1 Homo sapiens CDNA clone 123205 5'.					
ACCESSION	R00414					
NID	9750150					
KEYWORDS	EST.					
SOURCE	human clone-123205 library=Soares fetal liver spleen INFLS vector=PT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RI Rst162-Pac I Rst162-Eco RI liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dt) primer (5' AACCTGGAAGATATATTAAGAATCTTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT733 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Falma Bonaldo.					

ORGANISM	TITLE JOURNAL COMMENT
Homo sapiens	The Washu-Werch EST Project unpublished (1995)
Eucaryote: Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia	
Eutheria: Primates: Catarrhini: Hominoidea: Homo.	
REFERENCE	
AUTHORS	
1 (pages 1 to 359)	
Hillier, L., Clark, N., Dubaque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kuchida, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisksis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.	

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

High quality sequence stops: 312
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Location/Qualifiers
1. .359
/organism="Homo sapiens"
/clone="123205"

FEATURES

source

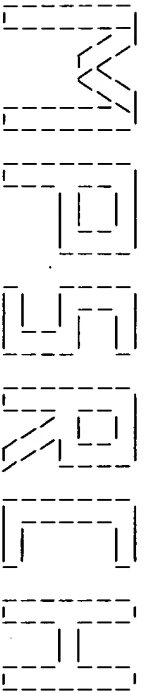
BASE COUNT 74 a 92 c 79 g 111 t 3 others
ORIGIN

Query Match 6.7%: Score 285; DB 5; Length 359;
Best Local Similarity 96.6%: Pred. No. 0.00e+00;
Matches 313; Conservative 0; Mismatches 7; Indels 4; Gaps 3;

Db 1 AGAATTTGAGTCAGAGAGAACGCTCTTGTGCTCTTGTGCTCTTGTGCTCTGTC 60
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OY 3729 AGAATTTGAGTCAGAGAGAACGCTCTTGTGCTCTTGTGCTCTGTC 3788
Db 61 CTTGGCAGGCTCCCTTTGGAGAGAGAGACACAGCCGGGTGTGTCTG 120
|||||
OY 3789 CTTGGCAGGCTCCCTTTGGAGAGAGAGAGACACAGCCGGGTGTGTCTG 3848
Db 121 CAGCACCGTGGGCTCTCAAGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCT 180
|||||
OY 3849 CAGCACCGTGGGCTCTCAAGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCT 3908
Db 181 TCTTCTCTCTTNCNAGAGCTACGCTACGTATGTATACGCGGCTCTCTCTCT 240
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OY 3909 TCTTCTCTCTTCTCTAG-ACGTACGCTACGTATGTATACGCGGCTCTCTCT 3967
Db 241 ACATATATGTATATACATCATCATATATATATATATATATATATATATAT 300
|||||
OY 3968 ACATATATGTATATACATCATCATATATATATATATATATATATATAT 4025
Db 301 TTTTAAAGGCAACAAACTATGG 324
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OY 4026 TTTTAAAG-CAACAAACTATGG 4048

Search completed: Thu Mar 11 22:08:09 1999
Job time : 13946 secs.

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(TM)

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Mparc_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Mar 11 22:08:32 1999; Masp time 667.91 Seconds

Tabular output not generated. 865.055 Million cell updates/sec

Title: >US-08-866-354-35
Description: (1-4232) from US0886354.seq
Perfect Score: 4232
N.A. Sequence: 1 CATGAGAAACCTCAGTANG.....AAGGCTCAATAAGCTGCG 4232
Comp: GTCCTCTTTGGAGTCATTC.....TTCCGAGGTTATTTCACGC

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 186442 segs, 68026449 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

n-geneseq2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 10.393; Variance 6.355; scale 1.635

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1884	44.5	1888 39	V00248	Human Ret ligand retl	0.00e+00
2	359	8.5	453 37	T84978	Human EST-derived seq	3.82e-219
3	295	7.0	351 37	T84978	Human EST-derived seq	4.75e-175
4	223	5.3	2138 38	T95297	Rat glial cell line-d	7.51e-126
5	223	5.3	3616 39	V00245	Rat Ret ligand retl	1.71e-124
6	221	5.2	2378 37	T84975	Rat glial cell derive	2.18e-118
7	212	5.0	2568 38	T88419	Human glial cell line	6.05e-111
8	201	4.7	201 37	T84980	Human EST-derived seq	6.05e-111
9	201	4.7	201 37	T84981	Human EST-derived seq	6.05e-111
10	161	3.8	1223 39	V00246	Human Ret ligand retl	4.53e-84
11	161	3.8	1682 39	V00247	Human Ret ligand retl	4.53e-84
12	121	2.9	840 37	T84977	Mouse GDNF alpha clo	1.23e-57
13	50	1.2	3000 38	V01547	Rat syntaxin 1B gene.	2.73e-13

14	46	1.1	65 29	T66072	(dc-da)n.(dc-dt)n pol	5.09e-11
15	46	1.1	65 29	T65724	Repeat sequence from	1.39e-11
16	47	1.1	72 29	T65729	(dc-da)n.(dc-dt)n pol	1.39e-11
17	47	1.1	72 29	T66078	Oligonucleotide probe	1.85e-10
18	45	1.1	91 9	O51746	Oligonucleotide repeat se	1.85e-10
19	47	1.1	91 9	O51746	Polymorphic repeat se	1.39e-11
20	47	1.1	194 29	T65666	Base substituted E.co	5.09e-11
21	46	1.1	204 1	N81164	Fragile X diagnostic	1.39e-11
22	47	1.1	219 4	O27094	Polymorphic repeat se	5.09e-11
23	46	1.1	264 29	T65661	Fragile X diagnostic	5.09e-11
24	46	1.1	266 4	O27097	Fragile X diagnostic	5.09e-11
25	48	1.1	282 4	O27100	Polymorphic repeat se	1.39e-11
26	47	1.1	387 29	T65695	Pemphigus vanhamel geno	1.39e-11
27	47	1.1	448 35	T66882	Viral infection gene	5.09e-11
28	46	1.1	835 38	V06122	Human RAdcompb cdna s	1.39e-11
29	47	1.1	1647 35	T91036	Human checkpoint gene	1.39e-11
30	47	1.1	1647 35	T91036	Mouse lactoferrin gen	5.09e-11
31	46	1.1	3054 7	O42406	Murine interleukin-17	1.85e-10
32	45	1.1	3288 23	T33800	Porphyrin-accumulatin	3.77e-12
33	48	1.1	3381 33	T78597	Porphyria-BamHI fragmen	3.77e-12
34	48	1.1	3383 28	T60965	Plasmid pUC19-SFG.	1.39e-11
35	48	1.1	3925 21	T13237	Retroviral vector MFG	1.39e-11
36	47	1.1	6350 23	T35198	PXS 741 insert contg.	1.39e-11
37	47	1.1	8045 17	T12237	PKS 741 insert contg.	1.39e-11
38	47	1.1	14704 3	O20685	Shuttle vector pAdel	1.85e-10
39	47	1.1	14704 3	O20685	Polymorphic repeat se	6.66e-10
40	45	1.1	19307 20	T27558	Base substituted E.co	6.66e-10
41	44	1.0	179 29	T65677	Rat cryptdin 3 gene.	6.66e-10
42	44	1.0	204 1	N81164	Partial sequence of m	6.66e-10
43	44	1.0	2551 22	T30738	Mouse SRY-related gen	6.66e-10
44	44	1.0	3812 2	O10991		
45	44	1.0	10266 22	T33007		

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	V00248 standard; cDNA; 1888 BP.	
AC	V00248:	
DT	21-MAY-1998 (first entry)	
DE	Human Ret ligand retl2 cDNA.	
KW	Ret ligand; Retl; Retl2; receptor; signal transduction; human;	
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;	
KW	kidney transplant; toxic injury; hypoxic injury;	
KW	neurodegeneration; motor neurone disease; multiple sclerosis;	
KW	infection; meningitis; myelopathy; Creutzfeldt-Jacob disease;	
KW	cerebral palsy; Lyme disease; muscular dystrophy;	
KW	myasthenia gravis; tumour; therapy; ss.	
OS	Homo sapiens.	
FH		
FT	key	Location/Qualifiers
FT	CDS	25..1419
FT		/*tag=a
PD	WO9744356-A2.	
PN	27-NOV-1997.	
PE	07-MAY-1997: U07726.	
PR	10-APR-1997: US-017427.	
PR	08-MAY-1996: US-017427.	
PR	07-JUN-1996: US-019300.	
PR	16-JUL-1996: US-021859.	
PA	(BIO) BIOGEN INC.	
PI	Cate RL, Hession C, Santicola-Nedel M;	
PI	WPI: 98-018431/02.	
PI	P-PSDB: W37460.	
PT	New nucleic acid encoding ret receptor ligands and related protei	
PT	- vectors, transformed cells and antibodies, used for promoting ce	
PT	growth and improving survival of injured cells, especially renal	
PT	nerve cells	
PS	Claim 1: Page 66-69, 113pp. English.	
CC	This sequence comprises cDNA coding for human Ret ligand (R...)	
CC	Retl2 (see W37460), a key component of the Ret signalling p...)	
CC	It was isolated from a human foetal liver cDNA library by screeni...	
CC	with probes (see T99532-33) based on an EST identified using rat	

OY 3363 GGACACACAGCTCTTCCCAAGCTGCCACTCTGTGGGACCCGCTGGGGGCTGGCAGAG 3422
 Db 1861 ggcacgctcagcggcggcagcggcgtc 1888
 |||||||
 OY 3423 GGCATCGGTACGCGGGGACCGGGGCTG 3450

RESULT 2

ID T84979 standard; DNA: 453 BP.

AC T84979;

DT 27-APR-1998 (first entry)

DE Human EST-derived sequence y170a10.r1.

KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;

KM GDNF; human; kidney disease; glomerulonephritis; therapy;

OS expressed sequence tag; EST; ss.

PN Homo sapiens.

PM MO9733912-A2.

PD 18-SEP-1997.

PF 13-MAR-1997; U04363.

PR 14-MAR-1996; US-618236.

PA 14-MAR-1996; US-615902.

PI (GETH) GENENTECH INC.

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

DR WPI: 97-470819/43.

PT Isolated glial cell derived neurotrophic factor receptor alpha -

PT useful to develop products to diagnose and treat associated

PT disorders, particularly enteric nervous system or kidney disorders

PS Example 1; Page 61; 100pp; English.

CC This DNA sequence comprises a human EST-derived sequence designated

CC y170a10.r1. It can be used to identify glial cell derived

CC neurotrophic factor receptor (GDNFR) sequences, including human

CC variants. Also suitable as probes for GDNFR sequences are another

CC human EST-derived sequence designated yeb3h05.r1 (see T84978), and

CC fragments of these EST-derived sequences (see T84980-81) or

CC proteins encoded by them. The invention relates to novel uses of

CC GDNFR and its receptor. In particular, it relates to native rat

CC (GDNFR alpha (see W27327), its variants and soluble derivatives

CC (extracellular domain), chimeric GDNFR alpha and antibodies which

CC bind to the GDNFR alpha, including agonist and neutralizing

CC antibodies, as well as various uses for these molecules. It also

CC relates to assay systems for detecting ligands to GDNFR alpha,

CC systems for studying the physiological role of GDNF, diagnostic

CC techniques for identifying GDNF-related conditions, methods for

CC identifying molecules homologous to GDNFR alpha, and claimed

CC methods for the treatment of GDNF-related and GDNFR alpha-related

CC conditions, particularly kidney disease associated with

CC glomerulonephritis and enteric nervous system related disorders.

CC Transgenic and knockout animals are also claimed.

SQ Sequence 453 BP: 86 A; 152 C; 121 G; 91 T;

Query Match 8.5%; Score 359; DB 37; Length 453;

Best Local Similarity 95.6%; Pred. No. 3,82e-219;

Matches 433; Conservative 0; Mismatches 9; Indels 11; Gaps 11;

Db 1 gcaacccatctcctgagatcgcgcgaagcgcgcgaacctgaatgaactgaagaagctgc 60

OY 2059 GCAACCATTTCTGCGATGCGTCCCAAGGCTGCAACCTGATGACAACTGCAAGAAGTGC 2118

Db 61 gctctctctacatctccatctgcaaccgcgaatctgcgcacgcgagcgtgcaacgcgc 120

OY 2119 GCTCTCTCTACATCTCCATCTGCACCGCGATCTCGCCACCGACGCTGCAACGGCC 2178

Db 121 gcaagtgcccaagggcctcgcgcgaatcttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180

OY 2179 GCAAGTGCCCAAGGCGCTCGCCAGTCTTTCGACCGGGTGGCCAGGGAATTAACCTACC 2238

Db 181 gcatgctctctcctcctcgcgaagaacgagcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240

OY 2239 GCATGCTCTTCTGCTCTGCGACAGACCGGTGCGCTGAGCGCGCGGCAACCATCC 2298

Db 241 tgcgcagctcctccatagagcaagaagaacccaactcctgagacctgcgtggcgtgt 300

OY 2299 TGCCCACTCTCTCTATGAGAGCAAGGAAGCCCAACTGCTGAGACTCGTGGCGGTGT 2358

Db 301 ggcagctgacacacgtgtgctccgcgcgtcgcgcacattccatgcacattgtctcag 360
 |||||||
 OY 2359 GCGGACTACACACGTCGTGCTCGCTCCGCGCTGGCGACTT-CCATGCCAATT-GT-CCAG 2415
 Db 361 ccttcctcacaagcgggtaccacagcgtcgcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420
 |||||||
 OY 2416 CCT-CCACACAGACGG-TCACAG-CTGCCCT-GCGGACAAATT-ACCAGG-CGTGTCT-G 2468
 Db 421 ggccttctatgttgatgattgggttgcatt 453
 |||||||
 OY 2469 GGCTCTT-ATGCTGCATGATTGGGTTCACAT 2500

RESULT 3

ID T84978 standard; DNA: 351 BP.

AC T84978;

DT 27-APR-1998 (first entry)

DE Human EST-derived sequence yeb3h05.r1.

KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;

KM GDNF; human; kidney disease; glomerulonephritis; therapy;

OS expressed sequence tag; ss.

PN Homo sapiens.

PM WO9733912-A2.

PD 18-SEP-1997.

PF 13-MAR-1997; U04363.

PR 14-MAR-1996; US-618236.

PA 14-MAR-1996; US-615902.

PI (GETH) GENENTECH INC.

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

DR WPI: 97-470819/43.

PT Isolated glial cell derived neurotrophic factor receptor alpha -

PT useful to develop products to diagnose and treat associated

PT disorders, particularly enteric nervous system or kidney disorders

PS Example 1; Page 61; 100pp; English.

CC This DNA sequence comprises a human EST-derived sequence designated

CC yeb3h05.r1. It can be used to identify glial cell derived

CC neurotrophic factor receptor (GDNFR) sequences, including human

CC variants. Also suitable as probes for GDNFR sequences are another

CC human EST-derived sequence designated y170a10.r1 (see T84979), and

CC fragments of these EST-derived sequences (see T84980-81) or

CC proteins encoded by them. The invention relates to novel uses of

CC GDNFR and its receptor. In particular, it relates to native rat

CC (GDNFR alpha (see W27327), its variants and soluble derivatives

CC (extracellular domain), chimeric GDNFR alpha and antibodies which

CC bind to the GDNFR alpha, including agonist and neutralizing

CC antibodies, as well as various uses for these molecules. It also

CC relates to assay systems for detecting ligands to GDNFR alpha,

CC systems for studying the physiological role of GDNF, diagnostic

CC techniques for identifying GDNF-related conditions, methods for

CC identifying molecules homologous to GDNFR alpha, and claimed

CC methods for the treatment of GDNF-related and GDNFR alpha-related

CC conditions, particularly kidney disease associated with

CC glomerulonephritis and enteric nervous system related disorders.

CC Transgenic and knockout animals are also claimed.

SQ Sequence 351 BP: 77 A; 117 C; 96 G; 57 T;

Query Match 7.0%; Score 295; DB 37; Length 351;

Best Local Similarity 96.5%; Pred. No. 4.75e-175;

Matches 302; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 39 gcaagagcaacatgctgtagtctgcaagc 98

OY 2052 GCCAAGAGCAACATTGCTGATGCTGCAAGGCGCTGCAACCTGAATGACAACTGCAAG 2111

Db 99 aagctgcctcctctacatctccatctgcaaccgcgaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 158

OY 2112 AAGCTGCGCTCTCTGATCTCATCTGCAACCGCGAGATTCGCCCAACGAGCGCTGC 2171

Db 159 aacgcgcgaagtgcacaagcgcctgcgcgaatctcttcgacgcgggtgcgcgcgcgcgcgcgcgcgc 218

OY 2172 AACCGCGCGAAGTGCACCAAGGCGCTGCGCCAGTCTTTCGACCGGGTGCACGAGGATAC 2231

KW GDNF: human; kidney disease; glomerulonephritis; therapy; EST;
KM expressed sequence tag; ss.
OS Homo sapiens.
PN WO9733912-A2.
PD 18-SEP-1997.
PR 13-MAR-1997; U04363.
PR 14-MAR-1996; US-618236.
PR 14-MAR-1996; US-615902.
PA (GETH) GENENTECH INC.
PI Klein RD, Moore MW, Rosenthal A, Ryan AM;
DR WPI: 97-470819/43.
PT Isolated glial cell derived neurotrophic factor receptor alpha -
PT useful to develop products to diagnose and treat associated
PT disorders, particularly enteric nervous system or kidney disorders
PS Example 1: Page 61; 100pp; English.
CC This DNA sequence comprises a fragment of a human EST-derived
CC sequence designated Y170a10.r1 (see T84979). It can be used as
CC a probe to identify glial cell derived neurotrophic factor receptor
CC (GDNFR) sequences, including human variants. The invention relates
CC to novel uses of GDNF and its receptor. In particular, it relates
CC to rat GDNFR alpha (see W27327), its variants and soluble derivatives
CC (extracellular domain), chimeric GDNFR alpha and antibodies which
CC bind to the GDNFR alpha, including agonist and neutralising
CC antibodies, as well as various uses for these molecules. It also
CC relates to assay systems for detecting ligands to GDNFR alpha,
CC systems for studying the physiological role of GDNF, diagnostic
CC techniques for identifying GDNF-related conditions, methods for
CC identifying molecules homologous to GDNFR alpha, and claimed
CC methods for the treatment of GDNF-related and GDNFR alpha-related
CC conditions, particularly kidney disease associated with
CC glomerulonephritis and enteric nervous system related disorders.
CC Transgenic and knockout animals are also claimed.
SQ Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;

Query Match 4.7%; Score 201; DB 37; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.05e-111;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gcaaccattgctgagatctgccaagagctgcaacctgatactgcaagaagctgc 60
|||
Oy 2059 GCAACCATGCTGATGATGTCGCAAGGCTGCACTGATGATGCAAGAGAGCTGC 2118
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 61 gctcctctacatctccatctgcaacgcgagatctgcccacgcgctgcacgcgc 120
Oy 2119 GCTCCTCTACATCTCCATCTGCAACCGCGAGATCTGCCCAACGAGGCTGCACACCCGC 2178
Db 121 gcaatgccaagaagcctctgcgcagcttcttcgacgggtgcccagagatcacctacc 180
Oy 2179 GCAATGCCACAAAGCCCTGCGCCCAATTCTTGACGGGTGCCGACGATACACTACCC 2238
Db 181 gcatgctctctctgctcctgcgc 201
Oy 2239 GCATGCTCTTCTGCTGCTGC 2259

RESULT 10
ID V00246 standard; cDNA; 1223 BP.
AC V00246;
DT 21-MAY-1998 (first entry)
DE Human Ret ligand retl1 partial cDNA.
KW Ret ligand; RetL; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebellar palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy; ss.
OS Homo sapiens.
FH CDS Location/Qualifiers
FT CDS 1..1041
FT CDS /*tag= a
PN WO9744356-A2.

PD 27-NOV-1997.
PF 07-MAY-1997; U00726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOU) BIOGEN INC.
PI Cate RL, Heaslon C, Santicola-Nadel M;
DR WPI: 98-018431/02.
DR P-PSDB: M37458.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 1: Page 58-60; 113pp; English.
CC This sequence comprises a partial cDNA for human Ret ligand (RetL)
CC RetL (see M37458), a key component of the Ret signalling pathway.
CC It was isolated from a human embryonic kidney cDNA library using
CC rat RetL cDNA (see V00245) as probe. A full-length sequence (see
CC V00247) for human RetL cDNA has also been obtained, as well as
CC mouse and human RetL2 and RetL3 sequences (see V00248-51). Vectors
CC containing RetL DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of RetL. Its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide,
CC RetL, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving
CC peripheral nervous system (Lyme disease, muscular dystrophy, etc.
CC myasthenia gravis). Fusion proteins are used to deliver
CC etc. to Ret-expressing cells, especially tumours.
SQ Sequence 1223 BP; 323 A; 329 C; 274 G; 297 T;

Query Match 3.8%; Score 161; DB 39; Length 1223;
Best Local Similarity 65.6%; Pred. No. 4.53e-84;
Matches 434; Conservative 0; Mismatches 219; Indels 5;

Db 89 ccaaaaggaaacaactgctcgatgacggaaggctgcaacctgcagacattgcaaa 120
|||
Oy 2053 CCAAGACAACCATGCTGCTGATGCTGCCAAGGCTGCACTGATGATGCAACAGTCAAGA 2118
Db 149 agtcagatgctggtatatacaaccgcgtgca-ccaacagcg-t-gtccaagatgctcgtc 200
|||
Oy 2113 AGCTGCGCTCTCTTACATCTCCATCTGCAACCGCGAGATCTGCCCAACGAGCTGCA 2178
Db 206 accgcgcgaagtgcacaagaagccctccgcgagttctctgcaagaaggtccgcgaac 2118
|||
Oy 2173 ACCGCGCCCAAGTGCACAAAGCCCTGCGCCCAATTCTTGACACGGGTGCCACAGCA 2238
Db 266 gctacggaatgctctctgctcctcgcgcgagacatgcctgcgacaagcgagagca 2718
|||
Oy 2233 CCTACCGCATGCTCTCTGCTGCTGCGCAAGACCAAGCGCTGCGTACAGCGCGCGCA 2293
Db 326 ccatcgctgctgtgtgctcctctatgaaagagggagagcccaactgcttgaattgca 2343
|||
Oy 2293 CCATCCGCGCCCAAGTGTCTCTATGAGACCAAGGAGAGCCCACTGCTGAGCTGCA 2353
Db 386 actcctgcaagaagaatatacatctgcagatctgcgctctgagatttttaccacacgt 2412
|||
Oy 2353 GCGTGTGCGGACACTGACACACTGTGTGCTGCTGCGGCTGCGGCACTTCCATCCCA 2472
Db 446 agccaagatcaaggtctgtcagcagctgtctaaagaaactacgctgactgctcctgc 505
|||
Oy 2413 GAGCGCTCTACACAGAGGTGACCAAGCTGCGCTGGGAGCAATTACAGAGCTGTGTGG 563
|||
Db 506 cctactcgaggcttatctggcagcagtcacaccccaactacatagactcagtagc-ct- 563
|||

QY 2473 CTTATCTGCGATGATTGGTTGACATGACACCTACTATGTGACTCCAGCCACATG 2532
 Db 564 -ca- gttg-tggcccatggtgactgacgacagtgagaaagcctagaagatgct 619
 QY 2533 GCATCTGTGGTGTCCCTCGTGTGACGTGTGCGACGGGAACATGAGAGAGATGTG 2592
 Db 620 tgaatttttgaattcttcctcaagacaatacatgcttaaaaaatgcaatccaagcttg 679
 QY 2593 AGAAGTTCCTCAGGACTTACCGAGACCAATGCTCCGGAAAGCGCATTCACAGCTTTG 2652
 Db 680 gcaatgctccgagtgtgacgctgtgacgacgcttcccaagacagaccacacgcga 739
 QY 2653 GCACACGGCAGAACGTGAACGTGTCCCAAAAAGGCCCTCTTCCAGCGCCACCCAGGCC 2712
 Db 740 ct 741
 QY 2713 CT 2714

RESULT 11
 ID V00247 standard; cDNA: 1682 BP.
 AC V00247:
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand retL cDNA.
 KW Ret ligand; RetL; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; nerve failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebellar palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy; ss.
 OS Homo sapiens.
 FT Key location/Qualifiers
 FT CDS 118..1500
 FT /tag- a
 PN WO97/4356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nedel M:
 DR MPI: 98-018431/02.
 DR P-PSDB; W37459.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 1: Page 62-64; 113pp: English.
 CC This sequence comprises cDNA coding for human Ret ligand (RetL)
 CC RetL (see W37459), a key component of the Ret signalling pathway.
 CC It was deduced from 2 clones isolated from human foetal kidney
 CC cDNA using primers based on a partial human retL cDNA (see
 CC V00246). Rat retL and mouse and human retL and retL3 sequences
 CC have also been identified (see V00245 and V00248-51). The human
 CC retL cDNA is 88.2% identical to rat retL cDNA. Vectors
 CC containing retL DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of RetL, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple
 CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
 CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
 CC cranial nerve or spinal cord injury, developmental disorders such
 CC as Down's syndrome and cerebral palsy, or conditions involving the
 CC peripheral nervous system (Lyme disease, muscular dystrophy and

CC myasthenia gravis). Fusion proteins are used to deliver RetL
 CC etc. to Ret-expressing cells, especially tumours.
 SQ Sequence 1682 BP; 417 A; 461 C; 433 G; 371 T;
 Query Match 3.8%; Score 161; DB 39; Length 1682;
 Best Local Similarity 65.6%; Pred. No. 4,536-84;
 Matches 434; Conservative 0; Mismatches 219; Indels 9; Gaps

Db 548 ccaaaagggaacacacgctgcatgaggaagcctgtaacatcgagacattgcaaa 607
 QY 2053 CCAAGAGCAACCATTTGCTTGATGCTGCCAAGGCTGCAACCTGAATACACTGCACGA 2112
 Db 608 agtaaggtcggcggtacatacaccgctgca-ccacaagc-g-t-gtccagatgtctga 604
 QY 2113 AGCTGGCTCCCTCCATCATCTCATCTCCAAACCGGGAATCTCGCCACCGAGCGTGA 2172
 Db 665 accgcgcgaagtgcacaaagccctcgagcttccttgacaaggtccgcgcaagcaca 724
 QY 2173 ACCGCCGCAAGGCGCACAAAGGCCCTGCGCATTTCTTGACCGGCTGCCAGCGATCA 2232
 Db 725 gctaggaatgctcttctgctccttgccggagcatcgtctcacagaagcggagcgaca 784
 QY 2233 CTTACCGCATGCTCTTGTGCTCTGCTCCAAAGCACAGCGCTGGCTGAGCGCGCGCAA 2292
 Db 785 ccacgtgcctgtgtgctcctataagaagaaggaagcccaactgtttgaattgcag 844
 QY 2293 CCATCTCCGCCACGCTGCTCTCATGAGCAAGAGAACCCCACTGCTGACACTGCTG 2352
 Db 845 actcctgaagaagcaattacatctgcagatctgccttgcggaattttttaccactgcc 904
 QY 2353 GCGTGTGCGGACTGACACCATCGTGTGCGTCCGCTGCGGCTGCGGACTTCATGCAATTGTC 2412
 Db 905 agccagagtcacagctctgtcagcagctgtctcaaggaataactagctcagctccctcg 964
 QY 2413 GAGCTCTCTACCAAGCGGTCAACCACTGCTCCTGCGGCAATTCACGAGCGTGTGGCT 2472
 Db 965 cctactcggggcttatttgacacagtcacagaccccaactacatagacacagtagc-ct- 1022
 QY 2473 CTTATGCTGGCATGTATGGTTTGACATGACACCAATATATGTGACTCCAGCCCATG 2532
 Db 1023 -ca- gttg-tggcccatggtgactgacgacagtgagaaagcctagaagatgct 1078
 QY 2533 GCATCTGTGGTGTCCCTCGTGTGACGTGTGCGACGCGGGAACATGAGAGAGATGTG 2592
 Db 1079 tgaatttttgaattcttcctcaagacaatacatgcttaaaaaatgcaatccaagcttg 1138
 QY 2593 AGAAGTTCCTCAGGACTTACCGAGACCAATGCTCTCCGAAACGCCATCCAGGCTTTG 2652
 Db 1139 gcaatgctccgagtgtgacgctgtgacgacgcttcccaagacagaccacacgcga 1198
 QY 2653 GCACACGGCAGAACGTGAACGTGTCCCAAAAAGGCCCTCTTCCAGCGCCACCCAGGCC 1258
 Db 1199 ct 1200
 QY 2713 CT 2714

RESULT 12
 ID T84977 standard; cDNA: 840 BP.
 AC T84977:
 DT 27-APR-1998 (first entry)
 DE Mouse GDNF alpha clone 26.3' end.
 KW GDNF; mouse; kidney disease; glomerulonephritis; therapy; ss.
 OS Mus musculus.
 FT WO97/33912-A2.
 PD 18-SEP-1997.
 PE 13-MAR-1997: U04363.
 PR 14-MAR-1996: US-618936.
 PR 14-MAR-1996: US-618902.
 PA (GENE) GENENTECH INC.
 PI Klein RD, Moore MM, Rosenthal A, Ryan AM:
 DR MPI: 97-470819/43.

PT Isolated glial cell derived neurotrophic factor receptor alpha -
 PT useful to develop products to diagnose and treat associated
 PT disorders, particularly enteric nervous system or kidney disorders
 PS Example 1, Page 60-61; 100pp; English.
 CC This cDNA sequence comprises the 3' end of mouse full-length
 CC glial cell derived neurotrophic factor receptor alpha (GDNFR alpha)
 CC (see W27327) clone 26; the 5' end of the clone is given in
 CC rat GDNFR alpha cDNA (see T84975) as probe. The invention relates
 CC to novel uses of GDNF and its receptor. In particular, it relates
 CC to native rat GDNFR alpha (see W27327), its variants and soluble
 CC derivatives (extracellular domain), chimeric GDNFR alpha and
 CC antibodies which bind to the GDNFR alpha, including agonist and
 CC neutralising antibodies, as well as various uses for these
 CC molecules. It also relates to assay systems for detecting ligands
 CC to GDNFR alpha, systems for studying the physiological role of
 CC GDNF, diagnostic techniques for identifying GDNF-related conditions,
 CC methods for identifying molecules homologous to GDNFR alpha, and
 CC therapeutic techniques (claimed) for the treatment of GDNF-related
 CC and GDNFR alpha-related conditions, particularly kidney disease
 CC associated with glomerulonephritis and enteric nervous system
 CC related disorders. Transgenic and knockout animals are also
 CC claimed.
 SQ Sequence 840 BP; 205 A; 245 C; 200 G; 190 T;
 Query Match 2.9%; Score 121; DB 37; Length 840;
 Best Local Similarity 64.2%; Pred. No. 1,23e-57;
 Matches 341; Conservative 0; Mismatches 184; Indels 6; Gaps 4;
 Db 1 CCGCGCAAGTGCACAAAGCCCTCCAGGAGTCTTCGCAAGTCCGCAAGCAGCAGC 60
 |||||||
 QY 2175 CGCGCAAGTGCACAAAGCCCTCCAGGAGTCTTCGCAAGTCCGCAAGCAGCAGC 2234
 |||||||
 Db 61 TACGAGATGCTCTTCTGCTCCGAGAGTGCAGGAGAGGAGGAGGAGGAGGAGGAG 120
 |||||||
 QY 2235 TACGAGATGCTCTTCTGCTCCGAGAGTGCAGGAGAGGAGGAGGAGGAGGAGGAG 2234
 |||||||
 Db 121 ATGTCCTGTGTGCTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 |||||||
 QY 2295 ATCCGTGCGACAGTCTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2354
 |||||||
 Db 181 TCCGCAAGAGCAATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 |||||||
 QY 2355 GTGTCGCGAGTGCACACCTGTGTGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 2414
 |||||||
 Db 241 CCAGAGTCAAGTGTCTGAGCAAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 |||||||
 QY 2415 GCTCTCTACAG 2474
 |||||||
 Db 301 TACTGAG 357
 |||||||
 QY 2475 TATCTGTGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2534
 |||||||
 Db 358 A--GTG--TGGGCGCGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
 |||||||
 QY 2535 ATCTGTGTGTCTCCCTGT 2594
 |||||||
 Db 415 AAGTCTCTGAATTTCTTAAAGAGCAATGCTGTCTCAAAATGCAATGCAATGCAATGCA 474
 |||||||
 QY 2595 AAGTCTCTGAATTTCTTAAAGAGCAATGCTGTCTCAAAATGCAATGCAATGCAATGCA 2654
 |||||||
 Db 475 AATGTCTGTGAGTGTGAG 525
 |||||||
 QY 2655 AACGGCAG 2705
 |||||||

KW neurodegenerative disease; hormonal disorder; immunological dis
 OS Rattus sp.
 FT Key Location/Qualifiers
 FT CDS 21..1077
 FT FT /*tag= a
 FT /product= syntaxin 1B
 PN US5693476-A.
 PD 02-DEC-1997.
 PF 24-FEB-1995; 393985.
 PR 24-FEB-1995; US-393985.
 PA (SMRD) UNIV LEARNED STANFORD JUNIOR.
 PI Scheller RH.
 DR WPI; 98-031743/03.
 DR P-PSDB; W43419.
 PT Screening assay for modulators of syntaxin binding - using PCR b
 PT comprising binding site of syntaxin, for identifying drug
 PT for treating CNS disorders, neuro-degenerative diseases, etc
 PS Disclosure; Column 37-42; 57pp; English.
 CC This nucleotide sequence represents the gene encoding the rat
 CC 1B protein. The invention relates to a method for identifying
 CC capable of affecting the binding of a syntaxin-binding protein
 CC e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to syntaxin. The method
 CC comprises measuring the effect of the test compound on the extent of
 CC binding between the SBP and the SBP-binding site on syntaxin. The
 CC can be used for identifying drugs capable of inhibiting or stimulating
 CC neurotransmitter release at the active zones of presynaptic membranes,
 CC which may be useful for treating CNS disorders, affective or psychotic
 CC disorders, neurodegenerative diseases, hormonal or immunological
 CC disorders, tumours.
 SQ Sequence 3000 BP; 653 A; 863 C; 777 G; 707 T;
 Query Match 1.2%; Score 50; DB 38; Length 3000;
 Best Local Similarity 84.0%; Pred. No. 2,73e-13;
 Matches 68; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 Db 1815 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1873
 |||||||
 CP 957 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
 |||||||
 Db 1874 GT 1894
 |||||||
 CP 897 GT 877
 |||||||

RESULT 14
 ID T66072 standard; DNA; 65 BP.
 AC T66072;
 DT 18-JUN-1997 (first entry)
 DE (dc-da)n.(dg-dt)n polymorphic repeat sequence #9.
 KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.
 OS Homo sapiens.
 PN US5382979-A.
 PD 10-DEC-1996.
 PF 21-APR-1989; 341562.
 PR 21-APR-1989; US-341562.
 PR 05-SEP-1991; US-754351.
 PR 04-APR-1994; US-222177.
 PA (MARS-) MARSHFIELD CLINIC.
 PI Weber JL.
 DR WPI; 97-042299/04.
 PT Detection of polymorphic genetic markers of the form
 PT (dc-da)n.(dg-dt)n - using novel nucleic acid mols. as primers
 PS Example 8; Column 57-58; 186pp; English.
 CC The invention relates to the isolation of polymorphic repeat sequen
 CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
 CC markers. Primers based on these sequences can be used to detect
 CC repeats, especially for use in e.g. paternity or maternity testing,
 CC human genetic analysis such as linkage analysis or genetic diagnosis,
 CC commercial animal or plant breeding or pedigree analysis.
 CC The repeats, when analysed, fall into 4 categories:

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 WISE (TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:01:32 1999; Maspar time 16.46 Seconds

Tabular output not generated. 455.994 Million cell updates/sec

Title: >US-08-866-354-36
 Description: (1-464) from US08866354.pep
 Perfect Score: 3386
 Sequence: 1 MILANVFCLFFLDLTLNSL.....RAPSALTVLSVLMKRLAL 464

Scoring table:
 PAM 150
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a:geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29

Statistics: Mean 34.889; Variance 136.192; scale 0.256

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3383	99.9	464	W37460	Human Ret ligand RetL 0.00e+00	
2	1554	45.9	466	W35334	Rat Ret ligand RetL 2.14e-152	
3	1554	45.9	466	W37457	Rat Ret ligand RetL 2.14e-152	
4	1554	45.9	466	W27327	Rat Ret ligand RetL 2.14e-152	
5	1520	44.9	466	W35333	Human Ret ligand RetL 1.09e-148	
6	1499	44.3	460	W37459	Human Ret ligand RetL 2.11e-146	
7	1142	33.7	346	W37458	Human Ret ligand RetL 1.28e-107	
8	782	23.1	397	W37461	Mouse Ret ligand RetL 5.23e-69	
9	755	22.3	346	W37455	Mouse Ret ligand RetL 5.53e-66	
10	708	20.9	400	W37463	Human Ret ligand RetL 5.64e-61	
11	676	20.0	315	W37462	Human Ret ligand RetL 3.42e-57	
12	103	3.0	1712	R22461	Masking protein high 8.62e+00	
13	98	2.9	179	W21646	Tomato ACC synthase 7.20e+00	
14	99	2.9	483	R15509	Tyrosine synthase 7.20e+00	
15	99	2.9	4472	W22601	Beta 3 adrenergic rec 1.47e+01	
16	95	2.8	402	R06495	Human beta-3 adrenergic 1.47e+01	
17	95	2.8	408	R54991	Antigenic cysteine pro 2.97e+01	
18	91	2.7	342	R12089		

19	91	2.7	342	2	R12090	Antigenic cysteine pro 2.97e+01
20	93	2.7	485	3	R15508	Tomato ACC synthase e 2.09e+01
21	88	2.6	227	1	R04497	HIV fusion protein PB 4.98e+01
22	88	2.6	227	1	P94807	Pblm12 HIV fusion pr 4.19e+01
23	89	2.6	325	19	R91347	Murine PLAP, for redu 4.19e+01
24	89	2.6	325	17	R85872	MD-40 domain-contg. P 4.19e+01
25	89	2.6	325	5	R25074	PLAP 4.19e+01
26	89	2.6	362	16	R48695	G-protein coupled hum 4.19e+01
27	89	2.6	362	19	W02667	G-protein coupled hum 4.19e+01
28	88	2.6	520	10	R52831	Sequence of human alp 4.19e+01
29	87	2.6	520	10	R53072	Alpha 1b adrenergic r 4.19e+01
30	87	2.6	520	14	R85943	Alpha 1b adrenergic r 4.19e+01
31	89	2.6	814	21	W11940	gd.trkA fusion us 4.19e+01
32	88	2.6	925	14	R79148	Human insulin recepto 4.19e+01
33	89	2.6	1404	8	R38304	Sequence of a serine 4.19e+01
34	86	2.5	226	3	R13757	Prolectin 4.19e+01
35	84	2.5	240	29	W23954	Chimeric humanised m 4.19e+01
36	85	2.5	650	1	P81137	Human protein S 4.19e+01
37	84	2.5	751	10	R53088	Human masking protein 4.19e+01
38	84	2.5	752	10	R53087	Human masking protein 4.19e+01
39	84	2.5	756	10	R53086	Human masking protein 4.19e+01
40	85	2.5	843	5	R27744	Extracellular protein 4.19e+01
41	84	2.5	845	10	R53089	Human masking protein 4.19e+01
42	84	2.5	1355	3	R14584	TGF beta 1 binding pr 4.19e+01
43	84	2.5	1830	8	R44504	Urea amide lyase 4.19e+01
44	85	2.5	4544	11	R60517	Human alpha-2-MR 4.19e+01
45	85	2.5	4544	9	R47861	Alpha 2-Macroglobulin 4.19e+01

ALIGNMENTS

RESULT 1
 ID W37460 standard; Protein: 464 AA.
 AC W37460;
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL2.
 KW Ret ligand; RetL; RetL2; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplants; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (Bio) BIOGEN INC.
 PI Cate RL, Hesslon C, Sanicola-Nadel M;
 DR N-PSDB: W00248.
 DR WPI: 98-018431/02.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 69-70; 113pp; English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL2,
 CC deduced from a cDNA clone (see W00248) isolated from a human foetal
 CC liver library. Ret and human RetL, and human and mouse RetL3
 CC sequences (see W37457-59 and W37461-63) are also claimed. Human
 CC RetL2 is 49.1% identical to human RetL protein. RetL is a
 CC key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL2 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL2, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.

CC RetL2, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and Wernicke's disease).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 464 AA:

Query Match 99.9%; Score 3383; DB 28; Length 464;
 Best Local Similarity 99.6%; Pred. No. 0.00e+00;
 Matches 462; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 mlanafeclffideltisalsapsalqgpehlywvrvpvcvranelcaaesncsarytl 60
 Oy 1 mlanafeclffideltisalsapsalqgpehlywvrvpvcvranelcaaesncsarytl 60
 Db 61 rclclgrdntmlankcegaalevqesplydcrcrkqmkkelqclqlywshlqtege 120
 Oy 61 rclclgrdntmlankcegaalevqesplydcrcrkqmkkelqclqlywshlqtege 120
 Db 121 efyeaspyevvrsrldfiflasifsgtadpvyasakshncidaekacnlndcklrs 180
 Oy 121 efyeaspyevvrsrldfiflasifsgtadpvyasakshncidaekacnlndcklrs 180
 Db 181 ysticnrelsptrcnrrckhkalrgfidvpselytymlfscqdgacaeerrigtlps 240
 Oy 181 ysticnrelsptrcnrrckhkalrgfidvpselytymlfscqdgacaeerrigtlps 240
 Db 241 cseyekexpcncldlgyvcrtdhlersrladfnancraayqvtscpadnyacislysgm 300
 Oy 241 cseyekexpcncldlgyvcrtdhlersrladfnancraayqvtscpadnyacislysgm 300
 Db 301 igfdmtpyvdsapglvswpcscrgsqgmeeceekflrdftempcrlnaqafngtd 360
 Oy 301 igfdmtpyvdsapglvswpcscrgsqgmeeceekflrdftempcrlnaqafngtd 360
 Db 361 vnvspkgsfsgatqgprvekpslpddsdstslgsvlytctavqegglkannskelam 420
 Oy 361 vnvspkgsfsgatqgprvekpslpddsdstslgsvlytctavqegglkannskelam 420
 Db 421 cftelttlngsnkvikpnsgrsarpasaltvslmklal 464
 Oy 421 cftelttlngsnkvikpnsgrsarpasaltvslmklal 464

RESULT 2
 ID W35334 standard; Protein: 468 AA.

AC W35334 (first entry)
 DT 01-MAY-1998
 DE Rat glial cell line-derived neurotrophic factor receptor.
 KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.
 OS Rattus sp.
 PN M09740152-A1.
 PD 30-OCT-1997.
 PE 15-APR-1997; U06281.
 PR 14-APR-1997; U06281.
 PR 22-APR-1996; U06281.
 PR 09-MAY-1996; U06281.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jang S, Men D;
 DR WPI: 97-535836/49.
 DR N-PSDS: T95297.
 PT Glial cell line derived neurotrophic factor receptor - useful to

PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and
 PT Alzheimer's disease
 PS Claim 1: Pages 96-98; 196pp; English.
 CC The present sequence is the rat glial cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or amyotrophic lateral sclerosis, complications of diabetes
 CC and Huntington's disease and (optionally in combination with GDNF)
 CC glaucoma, retinal degeneration and hearing loss caused by injury to
 CC inner ear sensory neurons. The receptor can also be used to block
 CC unwanted GDNF activity, analyse GDNF related molecules and
 CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
 CC cells, preferably transfected ex vivo, can be used similarly by
 CC implantation, and the use of the receptor cDNA in gene therapy is
 CC also contemplated. Probes based on the cDNA can be used to identify
 CC GDNF responsive cells and tissues, e.g. to identify patients who
 CC would benefit from GDNF therapy, and abnormalities in receptor
 CC expression, and to isolate molecules that form a complex with the
 CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
 CC antibodies, oligonucleotides derived from the cDNA and animal
 CC models that overexpress the receptor can be used to study the
 CC biological function of GDNF, knockout transgenic animals can be
 CC used to detect GDNF dependent neurons or processes and the anti-
 CC can be used in immunoassays for the receptor. The receptor can be
 CC GDNF specifically and with high affinity, acting as part of a
 CC complex that mediates/enhances signal transduction by GDNF.
 CC Increasing dopamine uptake in dopaminergic cells.
 CC Sequence 468 AA;

Query Match 45.9%; Score 1554; DB 28; Length 468;
 Best Local Similarity 48.2%; Pred. No. 2.14e-152;
 Matches 223; Conservative 102; Mismatches 120; Indels 36;

Db 2 flactylfaldplldlmaevsg-gdrldcvvasgqlkegscstkytltrcvagkknv 4
 Oy 12 fludturlslaspslqgelhgmrvpvcvranelcaaesncsarytlrclclgrdnt 7
 Db 61 slsgleakdeeraamealkgkslyncrcrkqmkkelqclqlywshlqtege 119
 Oy 71 tm---lank-bcqaalevlosplydcrcrkqmkkelqclqlywshlqtegefevns 120
 Db 120 pyepvnsrlsdifravpfsdvfgvehlsgkncldaaacnldctckkyrsalytpt 120
 Oy 127 pyepvnsrlsdifravpfsdvfgvehlsgkncldaaacnldctckkyrsalytpt 120
 Db 180 tsm-nevncnrrckhkalrgfidvpselytymlfscqdgacaeerrigtlps 180
 Oy 187 reispsternrckhkalrgfidvpselytymlfscqdgacaeerrigtlps 180
 Db 239 erpncldsgackcnylcrsladffncqgpesrvancnklenyadcllaysgllqcv 239
 Oy 247 EKPNCIDLRGVCRTDHLCRSLADFNHNCRASTYTVSCPADNYOALGSGAGMIGDHI 247
 Db 299 pnyvds-s-lsawpdcnsgndledclflnfikntclxnaiaqafngsdvcmwup 356
 Oy 307 PNYVDSSTGLVSPSCSCRGSGMEECEKFLDFTENCLRNAIOAFNGTWNVSPK 356
 Db 357 appvgtattatfrknpkplgageneplthvpcanlqgqklksnvsgthclsls 416
 Oy 367 GPSFOATQAPRV-E-KTPSLPDDLSSTS-IGTSVITTCSTVOROGKANNKSELSCFT 423
 Db 417 dsdfgkglagasehltks-ma-appscslslyvmltala 457
 Oy 424 E-LTTNIIPOSNNKVIKPNSGPSRARSALTIVSLMLK-LA 463

RESULT 3
 ID W37457 standard; Protein: 468 AA.
 AC W37457;
 DT 21-MAY-1998 (first entry)
 DE Rat Ret ligand RetL.
 KW Ret ligand; RetL; receptor; signal transduction; rat;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;

Query Match 45.98; Score 1554; DB 27; Length 468;
 Best Local Similarity 48.24; Pred. No. 2,14e-152;
 Matches 223; Conservative 102; Mismatches 120; Indels 18; Gaps 15;

Db 2 flaltlyfalplldllmsaevsg-gdrldcvkasdgclkegsctkyrtlrqcvagketnf 60
 12 fllddtrslaspslsgpdlhgmrrpvdvranelcaaesncssrrtltroclagadrn- 70
 Db 61 sltslgleakdeersamealkqkslyncrcrkqmkhekncrlrywmysgl-agnlldeds 119
 71 TM---LANK-ECOAALVLEDSPLDYDCRCRKMKRELQCIQIYWSIHGLTEGEFEFEYAS 126
 Db 120 pyepvnsrlsdifrvpfisdvfgqvehlpkgnncldaaacnlddckkyrsayltptc 179
 127 pyepvnsrlsdifrlasifsgtgadpvyvsaakshncldaaaknldnckrlrsysistcn 186
 Db 180 tsmv-nevncrrkchkalqfddkypakhsygmllfscrdiaeterritqlyvcsyeer 238
 187 REISPERENRRKCHALQFEDRVSEYTYRMLFCSCODQCAERRRQIILPSCSYEDK 246
 Db 239 erpncrlsdgscntyrcsrldaffincqpsrsvsnclkenyadcllaysgllgtmt 298
 247 ERKNCIDLGVCTDHLCHRLADFHANCRASYQVTSCPADNYQACLSYAGMIGFDMT 306
 Db 299 pnyvds-s-lavapwcdsngndleclkfnnfkdnclknalqafngsdvymwp 356
 307 PNVDSPTGIYVSPWCSGSGNMECEKFLRDTFENPCLRNALIOAFNGNTNVSXPK 366
 Db 357 apfvgttatttatlrvknkplpagseneipthvlppeanlqagllkenvsnthclis 416
 367 GSFQATQAPRV-E-KTPELPDLSSTS-LGTSVITTCISVQEGKANKNSKELSMCT 423
 Db 417 dsdfgkdglagaashltks-ma-appscglsplylvtal 457
 424 E-LTNIIPGSMKVIKPNSGPRARPSALTIVLSVLMK-LA 463

RESULT 5
 ID W35333 standard; Protein: 465 AA.
 AC W35333;
 DT 01-MAY-1998 (first entry)
 DE Human glial cell line-derived neurotrophic factor receptor.
 KW Human: glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.
 OS Homo sapiens.
 PN W09740152-A1.
 PD 30-OCT-1997.
 PF 15-APR-1997; 006281.
 PR 14-APR-1997; US-837199.
 PR 22-APR-1996; US-015907.
 PR 09-MAY-1996; US-017221.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR N-PSDB: T88419.
 DR N-PSDB: T88419.
 PT glial cell line derived neurotrophic factor receptor - useful to
 treat dopaminergic nerve cell disorders, e.g. Parkinson's and
 Alzheimer's disease
 PS Claim 1: Pages 91-93; 196pp; English.
 CC The present sequence is the human glial cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or amyotrophic lateral sclerosis, complications of diabetes
 CC and Huntington's disease and (optionally) in combination with GDNF
 CC glaucoma, retinal degeneration and hearing loss caused by injury to
 CC inner ear sensory neurons. The receptor can also be used to block
 CC unwanted GDNF activity, analyse GDNF related molecules and
 CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
 CC cells, preferably transfected ex vivo, can be used similarly by
 CC implantation, and the use of the receptor cDNA in gene therapy is

CC also contemplated. Probes based on the cDNA can be used to identify
 CC GDNF responsive cells and tissues, e.g. to identify patients at
 CC would benefit from GDNF therapy, and abnormalities in receptor
 CC expression, and to isolate molecules that form a complex with
 CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
 CC antibodies, oligonucleotides derived from the cDNA and animal
 CC models that overexpress the receptor can be used to study the
 CC biological function of GDNF, knockout transgenic animals can be
 CC used to detect GDNF dependent neurons or processes and the antibody
 CC can be used in immunoassays for the receptor. The receptor binds
 CC GDNF specifically and with high affinity, acting as part of a
 CC complex that mediates/enhances signal transduction by GDNF, i.e.
 CC increasing dopamine uptake in dopaminergic cells.
 CC Sequence 465 AA;

Query Match 44.98; Score 1520; DB 28; Length 465;
 Best Local Similarity 48.18; Pred. No. 1.09e-146;
 Matches 222; Conservative 101; Mismatches 122; Indels 17; Gaps 15;

Db 2 flaltlyfalplldllmsaevsg-gdrldcvkasdgclkegsctkyrtlrqcvagketnf 60
 12 fllddtrslaspslsgpdlhgmrrpvdvranelcaaesncssrrtltroclagadrn- 70
 Db 61 slaslgleakdeersamealkqkslyncrcrkqmkhekncrlrywmysgl-agnlldeds 119
 71 TM---LANK-ECOAALVLEDSPLDYDCRCRKMKRELQCIQIYWSIHGLTEGEFEFEYAS 126
 Db 120 pyepvnsrlsdifrvpfisdvfgqvehlpkgnncldaaacnlddckkyrsayltptc 179
 127 pyepvnsrlsdifrlasifsgtgadpvyvsaakshncldaaaknldnckrlrsysistcn 186
 Db 180 tsmv-ndvncrrkchkalqfddkypakhsygmllfscrdiaeterritqlyvcsyeer 238
 187 REISPERENRRKCHALQFEDRVSEYTYRMLFCSCODQCAERRRQIILPSCSYEDK 246
 Db 239 erpncrlsdgscntyrcsrldaffincqpsrsvsnclkenyadcllaysgllgtmt 298
 247 ERKNCIDLGVCTDHLCHRLADFHANCRASYQVTSCPADNYQACLSYAGMIGFDMT 306
 Db 299 pnyvds-s-lavapwcdsngndleclkfnnfkdnclknalqafngsdvymwp 356
 307 PNVDSPTGIYVSPWCSGSGNMECEKFLRDTFENPCLRNALIOAFNGNTNVSXPK 366
 Db 357 apfvgttatttatlrvknkplpagseneipthvlppeanlqagllkenvsnthclis 416
 367 GSFQATQAPRV-E-KTPELPDLSSTS-LGTSVITTCISVQEGKANKNSKELSMCT 423
 Db 417 ngnyekglagaashltks-ma-appscglsplylvtal 455
 424 E-LTNIIP-GSMKVIKPNSGPRARPSALTIVLSVLMK-LA 464

RESULT 6
 ID W37459 standard; Protein: 460 AA.
 AC W37459;
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL.
 KW Human Ret; RetL; RetL; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; 007726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.

M P E R C H
(TM)

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Mparch_p protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Mar 8 14:03:59 1999; Maspar time 23.85 Seconds
Tabular output not generated. 728.716 Million cell updates/sec

Title: >US-08-866-354-36
Description: (1-464) from US08866354.pep
Perfect Score: 3386
Sequence: 1 MILANVFCLFFFLDDTLRLSL.....RAPSALTYLSVLMKIAL 464

Scoring table:
PAM 150
Gap 11

Searched: 116738 segs, 37463448 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r58
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 46.701; Variance 78.241; scale 0.597

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	782	23.1	397	2 JE0082	GPI-linked receptor -	1.79e-154
2	100	3.0	452	2 S68456	translation elongatio	1.84e-01
3	100	3.0	452	2 S62767	translation elongatio	1.84e-01
4	103	3.0	1712	2 A38261	masking protein precu	6.65e-02
5	95	2.8	113	2 C70927	probable rps protein	9.54e-01
6	96	2.8	201	2 A47096	response regulator ho	6.90e-01
7	96	2.8	344	2 S72723	dipeptide transport p	6.90e-01
8	95	2.8	408	1 QRH0BE	Beta-3-adrenergic rec	9.54e-01
9	95	2.8	414	1 ORH0B3	Beta-3-adrenergic rec	9.54e-01
10	90	2.7	189	2 E69410	acetoin utilization p	4.62e+00
11	91	2.7	342	2 A45524	cysteine protease (3.39e+00
12	91	2.7	342	2 A44665	cysteine protease (3.39e+00
13	91	2.7	352	2 A57164	major allergen Bla g	3.39e+00
14	91	2.7	428	2 S67176	tRNA isopentenyltrans	3.39e+00
15	93	2.7	452	2 S62768	translation elongatio	1.81e+00
16	90	2.7	568	2 S74481	probable phosphoester	4.62e+00
17	93	2.7	799	1 TVRTTB	nerve growth factor r	1.81e+00
18	91	2.7	879	1 ORRTLD	LDL receptor precurs	3.39e+00
19	92	2.7	1603	2 S17983	gene posterior sex co	2.48e+00
20	92	2.7	2410	1 Q17948	genome polypeptide 1	2.48e+00
21	92	2.7	2412	1 Q1537	genome polypeptide 1	2.48e+00
22	90	2.7	2907	2 A57278	fibrillin-2 precursor	4.62e+00
23	89	2.6	302	1 WZBE9	gene 9 protein - huma	6.27e+00

24	89	2.6	325	2 A40963	phospholipase A2-act1	6.27e+00
25 <td>89</td> <td>2.6<td>354</td><td>2 B56392</td><th>beta-galactoside alph</th><th>6.27e+00</th></td>	89	2.6 <td>354</td> <td>2 B56392</td> <th>beta-galactoside alph</th> <th>6.27e+00</th>	354	2 B56392	beta-galactoside alph	6.27e+00
26 <td>88</td> <td>2.6<td>379</td><td>2 A44473</td><td>UTP--hexose-1-phospha</td><td>8.50e+00</td></td>	88	2.6 <td>379</td> <td>2 A44473</td> <td>UTP--hexose-1-phospha</td> <td>8.50e+00</td>	379	2 A44473	UTP--hexose-1-phospha	8.50e+00
27 <td>88</td> <td>2.6<td>379</td><td>2 I57459</td><td>galactose-1-phosphate</td><td>8.50e+00</td></td>	88	2.6 <td>379</td> <td>2 I57459</td> <td>galactose-1-phosphate</td> <td>8.50e+00</td>	379	2 I57459	galactose-1-phosphate	8.50e+00
28 <td>88</td> <td>2.6<td>418</td><td>2 G02953</td><td>Beta-3-adrenergic rec</td><td>8.50e+00</td></td>	88	2.6 <td>418</td> <td>2 G02953</td> <td>Beta-3-adrenergic rec</td> <td>8.50e+00</td>	418	2 G02953	Beta-3-adrenergic rec	8.50e+00
29 <td>88</td> <td>2.6<td>432</td><td>2 DEM2MC</td><td>malate dehydrogenase</td><td>8.50e+00</td></td>	88	2.6 <td>432</td> <td>2 DEM2MC</td> <td>malate dehydrogenase</td> <td>8.50e+00</td>	432	2 DEM2MC	malate dehydrogenase	8.50e+00
30 <td>88</td> <td>2.6<td>463</td><td>2 A26652</td><td>Type I site-specific</td><td>8.50e+00</td></td>	88	2.6 <td>463</td> <td>2 A26652</td> <td>Type I site-specific</td> <td>8.50e+00</td>	463	2 A26652	Type I site-specific	8.50e+00
31 <td>88</td> <td>2.6<td>480</td><td>2 S60381</td><td>RPD3 protein homolog</td><td>8.50e+00</td></td>	88	2.6 <td>480</td> <td>2 S60381</td> <td>RPD3 protein homolog</td> <td>8.50e+00</td>	480	2 S60381	RPD3 protein homolog	8.50e+00
32 <td>87</td> <td>2.6<td>493</td><td>2 JC5621</td><td>epidermal growth fact</td><td>1.15e+00</td></td>	87	2.6 <td>493</td> <td>2 JC5621</td> <td>epidermal growth fact</td> <td>1.15e+00</td>	493	2 JC5621	epidermal growth fact	1.15e+00
33 <td>89</td> <td>2.6<td>503</td><td>4 S23741</td><td>hypothetical TPRT/TK</td><td>6.27e+00</td></td>	89	2.6 <td>503</td> <td>4 S23741</td> <td>hypothetical TPRT/TK</td> <td>6.27e+00</td>	503	4 S23741	hypothetical TPRT/TK	6.27e+00
34 <td>88</td> <td>2.6<td>621</td><td>2 S26691</td><td>serine protease (EC</td><td>8.50e+00</td></td>	88	2.6 <td>621</td> <td>2 S26691</td> <td>serine protease (EC</td> <td>8.50e+00</td>	621	2 S26691	serine protease (EC	8.50e+00
35 <td>89</td> <td>2.6<td>700</td><td>1 TVHUTT</td><td>nerve growth factor I</td><td>6.27e+00</td></td>	89	2.6 <td>700</td> <td>1 TVHUTT</td> <td>nerve growth factor I</td> <td>6.27e+00</td>	700	1 TVHUTT	nerve growth factor I	6.27e+00
36 <td>89</td> <td>2.6<td>808</td><td>1 VGBESM</td><td>glycoprotein B precu</td><td>6.27e+00</td></td>	89	2.6 <td>808</td> <td>1 VGBESM</td> <td>glycoprotein B precu</td> <td>6.27e+00</td>	808	1 VGBESM	glycoprotein B precu	6.27e+00
37 <td>89</td> <td>2.6<td>854</td><td>1 ORHYLD</td><td>LDL receptor precurs</td><td>6.27e+00</td></td>	89	2.6 <td>854</td> <td>1 ORHYLD</td> <td>LDL receptor precurs</td> <td>6.27e+00</td>	854	1 ORHYLD	LDL receptor precurs	6.27e+00
38 <td>88</td> <td>2.6<td>863</td><td>2 S41984</td><td>SLP1 protein - yeast</td><td>8.50e+00</td></td>	88	2.6 <td>863</td> <td>2 S41984</td> <td>SLP1 protein - yeast</td> <td>8.50e+00</td>	863	2 S41984	SLP1 protein - yeast	8.50e+00
39 <td>88</td> <td>2.6<td>925</td><td>2 A39216</td><td>Plasma cell membrane</td><td>8.50e+00</td></td>	88	2.6 <td>925</td> <td>2 A39216</td> <td>Plasma cell membrane</td> <td>8.50e+00</td>	925	2 A39216	Plasma cell membrane	8.50e+00
40 <td>87</td> <td>2.6<td>1115</td><td>2 S64101</td><td>PAN2 protein - yeast</td><td>8.50e+00</td></td>	87	2.6 <td>1115</td> <td>2 S64101</td> <td>PAN2 protein - yeast</td> <td>8.50e+00</td>	1115	2 S64101	PAN2 protein - yeast	8.50e+00
41 <td>89</td> <td>2.6<td>1404</td><td>2 A36666</td><td>sestrate protein proc</td><td>8.50e+00</td></td>	89	2.6 <td>1404</td> <td>2 A36666</td> <td>sestrate protein proc</td> <td>8.50e+00</td>	1404	2 A36666	sestrate protein proc	8.50e+00
42 <td>89</td> <td>2.6<td>1408</td><td>2 S16148</td><td>gene sestrate protein</td><td>8.50e+00</td></td>	89	2.6 <td>1408</td> <td>2 S16148</td> <td>gene sestrate protein</td> <td>8.50e+00</td>	1408	2 S16148	gene sestrate protein	8.50e+00
43 <td>89</td> <td>2.6<td>2703</td><td>2 A24420</td><td>notch protein - fruit</td><td>8.50e+00</td></td>	89	2.6 <td>2703</td> <td>2 A24420</td> <td>notch protein - fruit</td> <td>8.50e+00</td>	2703	2 A24420	notch protein - fruit	8.50e+00
44 <td>88</td> <td>2.6<td>2871</td><td>2 A55567</td><td>fibrillin I - bovin</td><td>8.50e+00</td></td>	88	2.6 <td>2871</td> <td>2 A55567</td> <td>fibrillin I - bovin</td> <td>8.50e+00</td>	2871	2 A55567	fibrillin I - bovin	8.50e+00
45 <td>87</td> <td>2.6<td>2918</td><td>2 A54105</td><td>fibrillin-2 precursor</td><td>8.50e+00</td></td>	87	2.6 <td>2918</td> <td>2 A54105</td> <td>fibrillin-2 precursor</td> <td>8.50e+00</td>	2918	2 A54105	fibrillin-2 precursor	8.50e+00

ALIGNMENTS

RESULT	ENTRY	1	JE0082	#type complete
	ALTERNATE_NAMES		GPI-linked receptor - mouse	
	ORGANISM		GPI-linked receptor - mouse	
	DATE		21-May-1998	#sequence, revision 29-May-1998
	DATE		24-Sep-1998	#text, channel

ACCESSIONS	JE0082
REFERENCE	JE0082
#authors	Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
#journal	Biochem. Biophys. Res. Commun. (1998) 244:849-85.
#title	Molecular cloning and expression analysis of GPR110, a novel CDNA related to GPRalpha and NTRalpha.

#accession	JE0082
#molecule-type <td>MRNA</td>	MRNA
#residues <td>1-397</td>	1-397
#cross-references <td>DBP:AB008833; NID:Q2627159; PID:Q2627160</td>	DBP:AB008833; NID:Q2627159; PID:Q2627160
COMMENT	This protein plays a distinct role in cell survival and differentiation.

KEYWORDS

FEATURE	1-25
92.145.306	#domain signal sequence #status predicted #label signal
	#region hydrophobic
	#binding-site carbohydrate (Asn) (covalent) #status

SUMMARY	#length 397	#molecular-weight 44307	#checksum 2962
Query Match	23.1%	Score 782; DB 2; Length 397;	
Best local Similarity	38.2%	Pred. No. 1.79e-154;	
Matches 123;	Conservative 78;	Mismatches 96;	Indels 25; Gaps 18;

DB	41	CTGARKKCEANPACKAYOHLSCTSSLRPLLESANSADCLEAEDLRNSLIDRC	100
QY <td>40</td> <td>CVANELCAAESNCSRYRTLRCLAGRDRNTL--ANK--ECQALLEVLOEPLVDCRC<td>95</td></td>	40	CVANELCAAESNCSRYRTLRCLAGRDRNTL--ANK--ECQALLEVLOEPLVDCRC <td>95</td>	95
DB <td>101</td> <td>HRMKKQATCDDIYVHVHPRASIGDEL-DVSYEDTV--SKPKM-NL-S-K-LN-NL<td>152</td></td>	101	HRMKKQATCDDIYVHVHPRASIGDEL-DVSYEDTV--SKPKM-NL-S-K-LN-NL <td>152</td>	152
QY <td>96</td> <td>KRMKKELCQLQYVSHIGLGE-EFYEASYPEVTSRLSDIFLASIFSGTADPAV<td>154</td></td>	96	KRMKKELCQLQYVSHIGLGE-EFYEASYPEVTSRLSDIFLASIFSGTADPAV <td>154</td>	154
DB <td>153</td> <td>KPDSDLKFAMLCTHDKCDRLKRAYEACS-GI-----RCQHLCLAOULRSFEKAAS<td>207</td></td>	153	KPDSDLKFAMLCTHDKCDRLKRAYEACS-GI-----RCQHLCLAOULRSFEKAAS <td>207</td>	207
QY <td>155</td> <td>SASNNCLDAKACNLDNCKLRSSYISICNEISPTERCNRKHKALROFDPVPSE<td>214</td></td>	155	SASNNCLDAKACNLDNCKLRSSYISICNEISPTERCNRKHKALROFDPVPSE <td>214</td>	214
DB <td>208</td> <td>HAQGLLCPAPDAGCGERRNTIAPSCALPS-VTPNCLDLRSFCRADPLCRSLMDQ<td>266</td></td>	208	HAQGLLCPAPDAGCGERRNTIAPSCALPS-VTPNCLDLRSFCRADPLCRSLMDQ <td>266</td>	266
QY <td>215</td> <td>YTFMFLFCSC-QDOA-CAERRRQITLPSCSYEDKRPNCILDAGVCRDTDLCHSLADPH<td>272</td></td>	215	YTFMFLFCSC-QDOA-CAERRRQITLPSCSYEDKRPNCILDAGVCRDTDLCHSLADPH <td>272</td>	272

```

Db      267 THCPM-DIGTCATTEQR-CLARYGLGISTATPNEISVMYTVALS--CTCRSSGNLQ 322
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      273 ANCRASIOYVTSACADNYQNLCSGYAKMGIFDTPNIVDSPTGIWSPWCSCRSNGME 332
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      323 DECEQLERSEFSONPCLEVAIAA 344
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      333 ECEKFLRDFTPENPCLNRAIOA 354
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT          2
ENTRY           S68466
TITLE           translation elongation factor Tu-like protein P43 precursor,
                 mitochondrial - human
ORGANISM        Homo sapiens #common_name man
DATE            17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                28-Aug-1998

ACCESSIONS     S68466; S78551; I53499
REFERENCE       Wells, J.; Henkler, F.; Leversha, M.; Koshy, R.
#authors        FEBS Lett. (1995) 358:119-125
#journal         A mitochondrial elongation factor-like protein is
#title           over-expressed in tumours and differentially expressed in
                 normal tissues.
#accession       S68466
#molecule_type mRNA
#residues        1-452 ##label WEL
#cirs-references EMBL:S75463; NID:9833998; PID:9833999
#experimental_source liver
#note            It is uncertain whether Met-1 or Met-4 is the initiator
#accession       S78551
#molecule_type protein
#residues        57-65;239-270;352-361 ##label WES

GENETICS
#gene            GDB:P43
##cirs-references GDB:631149
#map_position    16p12-16p11.2
#genome          nuclear
CLASSIFICATION  superfamily translation elongation factor Tu: translation
                 elongation factor Tu homology
KEYWORDS         GTP binding; mitochondrion; P-loop
FEATURE
61-187           #domain translation elongation factor Tu homology #label
                 EF1\
                 #region nucleotide-binding motif A (P-loop)\
                 #region GTP-binding NKXD motif\
                 #region GTP-binding SAK/L motif\
                 #domain translation elongation factor Tu homology #label
                 EF1\
67-74           #region nucleotide-binding motif A (P-loop)\
184-187         #region GTP-binding NKXD motif\
219-221         #region GTP-binding SAK/L motif\
73,74,110,184,185,
187,219         #binding_site Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser)
SUMMARY          #length 452 #molecular_weight 49533 #checksum 1798

Query Match      3.0%: Score 100; DB 2; Length 452;
Best Local Similarity 27.6%: Pred. No. 1,84e+01;
Matches 21; Conservative 19; Mismatches 31; Indels 5; Gaps 4;

Db      231 LGLSVKVLDAVDYIIPVARDLERFLLPVAVYSVGREGVTYGTGLERILKKSGDEC 290
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      114 LGTNEGEEFYEA-SPEYPVTSR-LSDIFRLA--SIRSGAGAPVVSAXSNH-CLDAAKAC 168
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      291 ELFGHSKNRTVVIGI 306
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      169 NLNDCKRRLRSSYSISI 184
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT          3
ENTRY           S62767
TITLE           *type complete
                 translation elongation factor EF-Tu precursor - human
ORGANISM        Homo sapiens #common_name man
DATE            24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change
                28-Aug-1998

ACCESSIONS     S62767
REFERENCE       Worlax, V.L.; Burkhart, W.; Spremulli, L.L.
#authors        Worlax, V.L.; Burkhart, W.; Spremulli, L.L.
```

```

#journal      Blochlin. Biophys. Acta (1995) 1264:347-356
#title        Cloning, sequence analysis and expression of mammalian
               mitochondrial protein synthesis elongation factor Tu.
#accession    S62767
#status       preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues     1-452 ##label MOR
#cross-references EMBL:L38995; NID:g704415; PID:g704416
GENETICS
#genome       nuclear
CLASSIFICATION #superfamily translation elongation factor Tu; translation
                elongation factor Tu homology
KEYWORDS       GTP binding; mitochondrion; P-loop
FEATURE
58-184         #domain translation elongation factor Tu homology
                EPI\
64-71          #region nucleotide-binding motif A (P-loop)\
181-184        #region GTP-binding NKXD motif\
219-221        #region GTP-binding SAK/L motif\
70,71,107,181,182,
184,219        #binding_site Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asn)
                #status predicted
SUMMARY        #length 452 #molecular-weight 49540 #checksum 1000000000

Query Match      3.0%; Score 100; DB 2; Length 452:
Best Local Similarity 27.68; Pred. No. 1,84e-01;
Matches 21; Conservative 19; Mismatches 31; Indels 5; Gaps 0;

Db 231 LGKSYVKLLDAVDYTPVPAARLEPFLLPEAVSYSPGRGTVTGLERGLK...
OY 114 LGLEGESEFEHA-SPEEPTSR-LSDFRFLA--SIFSGTGADPVYSASNSH-CLDAK...
OY 169 NLNDCKKRLRSYISI 184

Db 291 ELGLSKNIRTVVTGI 306
OY 169 NLNDCKKRLRSYISI 184

RESULT 4
ENTRY      A38261 #type complete
TITLE      masking protein precursor - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change
10-Sep-1997

ACCESSIONS A38261
REFERENCE   A38261
#authors    Tsubli, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8835-8839
#title      Molecular cloning of the large subunit of transforming growth
               factor type beta masking protein and expression of the mRNA
               in various rat tissues.
#cross-references M0ID:91062373
#accession  A38261
#status     preliminary
#molecule_type mRNA
#residues   1-1712 ##label T5U
#cross-references GB:M55431; NID:g207285; PID:g207286
CLASSIFICATION #superfamily LBL receptor ligand-binding repeat homology
SUMMARY        #length 1712 #molecular-weight 186598 #checksum 9047

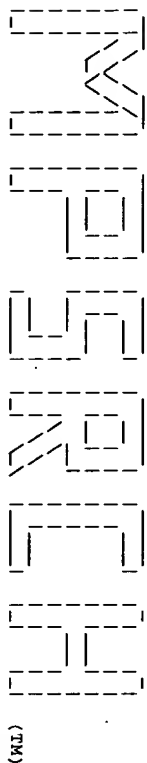
Query Match      3.0%; Score 103; DB 2; Length 1712:
Best Local Similarity 34.98; Pred. No. 6,65e-02;
Matches 15; Conservative 12; Mismatches 12; Indels 4; Gaps 4;

Db 1032 DECLDP-KVCT-NGSCNTLEGSYMCXCHKGYSP-T-P-DHRRCQ 1070
OY 159 NHCLDAKACNLNDNCKKRLRSYISICNKRNEIPTRCNRKACH 201

RESULT 5
ENTRY      C70927 #type complete
TITLE      probable rplis protein - Mycobacterium tuberculosis (strain
               H37RV)
ORGANISM   #formal_name Mycobacterium tuberculosis
```


PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 1: Page 79-80; 113pp: English.
CC This sequence comprises a partial cDNA clone, designated GJ128,
CC for human Ret ligand (RetL), RetL3 (see W37462), a key component of
CC the Ret signalling pathway. It was isolated from a human adult
CC heart cDNA library using a probe derived from a mouse RetL3 partial
CC cDNA (see V00256). A full-length sequence (see V00251) for human
CC RetL3 cDNA has also been obtained, as well as rat and human RetL1,
CC human RetL2 and mouse RetL3 sequences (see V00245-51). Vectors
CC containing RetL3 DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving the
CC peripheral nervous system (Lyme disease, muscular dystrophy and
CC myasthenia gravis). Fusion proteins are used to deliver toxins
CC etc. to Ret-expressing cells, especially tumours.
SQ Sequence 1271 BP; 264 A; 414 C; 316 G; 277 T;
Query Match 4.1%; Score 81; DB 39; Length 1271;
Best Local Similarity 98.8%; Pred. No. 5,61e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1184 ctggcctgtggtgctgtcttattctatttgcctaaagctctggtctctg 1243
Cp 84 CTGGAGCCTGTGGCCTTATTCTATTATGCTCTAAAGCTCTGGGCTCTTG 25
Db 1244 gatcatgattaaaccttgacct 1266
Cp 24 GATCATGATTAAACCTTGACTT 2
RESULT 6
ID V00251 standard; cDNA; 1699 BP.
AC V00251.
DT 21-MAY-1998 (first entry)
DE Human Ret ligand RetL3 cDNA.
KW Ret ligand; RetL; RetL3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 175..1377
FT /tag= a
FN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; 007726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
DR MPI: 98-018431/02.
P-PSDB: W37463.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell

PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 1: Page 82-84; 113pp: English.
CC This sequence comprises cDNA encoding human Ret ligand (RetL),
CC (see W37463), a key component of the Ret signalling pathway. It is
CC a composite of partial clone GJ148 (see V00250), obtained from an
CC adult heart cDNA library, and of clone GJ135, isolated from an
CC adult spinal cord cDNA library. Rat and human RetL1, human RetL2
CC and mouse RetL3 sequences are also claimed (see W37457-62). Vectors
CC containing RetL3 DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving the
CC peripheral nervous system (Lyme disease, muscular dystrophy and
CC myasthenia gravis). Fusion proteins are used to deliver toxins
CC etc. to Ret-expressing cells, especially tumours.
SQ Sequence 1699 BP; 328 A; 562 C; 468 G; 341 T;
Query Match 4.1%; Score 81; DB 39; Length 1699;
Best Local Similarity 98.8%; Pred. No. 5,61e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1612 ctggcctgtggtgctgtcttattctatttgcctaaagctctggtctctg 1671
Cp 84 CTGGAGCCTGTGGCCTTATTCTATTATGCTCTAAAGCTCTGGGCTCTTG 25
Db 1672 gatcatgattaaaccttgacct 1694
Cp 24 GATCATGATTAAACCTTGACTT 2
RESULT 7
ID V00256 standard; cDNA; 1878 BP.
AC V00256.
DT 21-MAY-1998 (first entry)
DE Mouse Ret ligand RetL3 cDNA partial clone (E87 AA50083).
KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 205..1245
FT /tag= a
FN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; 007726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
DR MPI: 98-018431/02.
P-PSDB: W37465.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Disclosure; Page 71-73; 113pp: English.



(TM)

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MParch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 03:17:56 1999; Maspar time 2882.03 Seconds

Tabular output not generated. 1237.127 Million cell updates/sec

Title: >US-08-866-354-37
Description: (1-1991) from US0886354.seq
Perfect Score: 1991
N.A. Sequence: 1 CAAGTCAGGTTTATCAT.....CATGATTAACCTTGACG 1991
Comp: GTTCAGTTTCCAAATTAGTA.....GTACTAATTGGAACTGAC

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0: Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum match 0%

Listing first 45 summaries

Database:

emb1-est56

Database:

genbank-est109

5:gb-est1 6:gb-est10 7:gb-est11 8:gb-est12 9:gb-est13
10:gb-est14 11:gb-est15 12:gb-est16 13:gb-est17
14:gb-est18 15:gb-est19 16:gb-est2 17:gb-est20
18:gb-est21 19:gb-est3 20:gb-est4 21:gb-est5 22:gb-est6
23:gb-est7 24:gb-est8 25:gb-est9 26:gb-est1 27:gb-est2
28:gb-est3 29:gb-est4

Statistics: Mean 11.743; Variance 2.290; scale 5.129

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
C 1	454	22.8	474	11	AA694259	213id11.s1 Soares feta 0.00e+00
C 2	428	21.5	450	21	W69774	z448g06.s1 Soares feta 0.00e+00
C 3	389	19.5	396	11	AA687725	nv08c06.s1 NCI_CGAP.Pr 0.00e+00
C 4	358	18.0	373	11	AA678356	z145901.s1 Soares feta 0.00e+00
C 5	352	17.7	436	21	W69813	z448g06.s1 Soares feta 0.00e+00
C 6	332	16.7	350	15	AA694036	oq02f02.s1 NCI_CGAP.Lu 0.00e+00
C 7	289	14.5	442	22	AA049894	mj1id08.s1 Soares feta 0.00e+00
C 8	232	11.7	465	11	AA050083	mj08d05.s1 Soares feta 0.00e+00
C 9	181	9.1	465	11	AA676213	z139h12.s1 Soares feta 0.00e+00
C 10	160	8.0	373	11	AA678356	z139h12.s1 Soares feta 0.00e+00
C 11	160	8.0	396	11	AA687725	nv08c06.s1 NCI_CGAP.Pr 0.00e+00
C 12	160	8.0	474	11	AA694259	z13id11.s1 Soares feta 0.00e+00
C 13	158	7.9	350	15	AA694036	oq02f02.s1 NCI_CGAP.Lu 0.00e+00

14	158	7.9	450	21	W69774	z448g06.s1 Soares feta 0.00e+00
15	152	7.6	353	21	AA041935	mj04d08.s1 Soares feta 0.00e+00
16	140	7.0	502	23	AA238748	my35d09.s1 Soares feta 0.00e+00
17	63	3.2	222	12	AA754459	97SN1787 Rice Immature 2.52e-10
18	63	3.2	252	12	AA754459	97SN1787 Rice Immature 2.52e-10
19	53	2.7	436	21	W69813	z448g06.s1 Soares feta 0.00e+00
20	48	2.4	247	12	AA754458	97SN1784 Rice Immature 2.52e-10
21	46	2.3	247	12	AA754458	97SN1784 Rice Immature 2.52e-10
22	39	2.0	478	21	W73581	z455h01.s1 Soares feta 0.00e+00
23	37	1.9	350	25	AA349976	EST35965 Infant brain 1.09e-11
24	34	1.7	189	11	AA676213	z139h12.s1 Soares feta 0.00e+00
25	33	1.7	431	18	AA179473	EST223187 Normalized r 6.00e-11
26	33	1.7	499	14	AA925330	UT-R-A1-ek-h-10-0-UI.s 1.09e-11
27	32	1.6	355	21	HS278350	H sapiens mRNA, expres 4.41e-11
28	31	1.6	415	17	AT073842	o011h09.s1 Soares feta 4.41e-11
29	31	1.6	419	20	HS278350	H sapiens partial cDN 4.41e-11
30	31	1.6	607	26	B16636	342P20.TPB C17978SKA1 4.41e-11
31	31	1.6	650	20	W27487	3194 Human retina cDNA 4.41e-11
32	32	1.6	2275	11	AF034173	Homo sapiens rRNA2 CO 1.09e-11
33	32	1.5	255	20	W46820	EST112821 Embryo, 8 we 2.52e-10
34	32	1.5	225	24	AA287263	0H56g10.s1 NCI_CGAP_G 2.52e-10
35	29	1.5	308	14	AA894529	EST19382 Retina II Hom 2.52e-10
36	29	1.5	321	24	AA317449	0236c11.s1 Soares feta 2.52e-10
37	29	1.5	396	17	AT080124	EST223927 Normalized r 2.52e-10
38	29	1.5	448	18	AT180186	Y775d11.s1 Homo sapien 2.52e-10
39	29	1.5	448	19	N58868	z189h09.s1 Soares feta 2.52e-10
40	29	1.5	467	11	AA705382	UT-R-A1-ek-h-10-0-UI.s 1.09e-11
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42	30	1.5	502	9	HS298510	ue96g10.Y1 Susano mus 1.09e-11
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44	29	1.5	618	26	FR0006945	Homo sapiens CAGL65 mr 2.52e-10
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ALIGNMENTS

RESULT 1 AA694259 474 bp mRNA EST 16-DEC-1997
LOCUS z13id11.s1 Soares fetal liver spleen INFUS S1 Homo sapiens CDNA
DEFINITION Clone 432405 3', mRNA sequence.
ACCESSION AA694259
NID 92695197
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 474)
REFERENCE
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact:
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40m3 fwd. ET from Amerisham
High quality sequence stop: 451.
Location/Qualifiers
1..474
/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: p77"
with a modified polylinker; Site: 1; Pac 1:
This is a subtracted version of the original
liver spleen INFUS library. 1st strand cDNA
with a Pac I - oligo(dT) primer [5'

ACTGGAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTZ3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo.
/db_xref="GDB:1332174"
/db_xref="taxon:9606"
/clone_1lb="32405"
/clone_1lb="Soares fetal liver spleen INFLS S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"

BASE COUNT 134 a 100 c 137 g 103 t

ORIGIN

Query Match 22.8% Score 454; DB 11; Length 474;
Best Local Similarity 99.8% Pred. No. 0.00e+00;
Matches 456; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 17 AGTCAAGGTTTATCATGATCCCAAGAGCCAGAGACTTTAGACATTAATAGGATA 76
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CP 1990 AGTCAAGGTTTATCATGATCCCAAGAGCCAGAGACTTTAGACATTAATAGGATA 1931
Db 77 AAGCAAGGCCACAGGCTCCAGCTCCTGATGCCAGATGTCGGCAGATCCGGGACAG 136
|||||
CP 1930 AAGCAAGGCCACAGGCTCCAGCTCCTGATGCCAGATGTCGGCAGATCCGGGACAG 1871
Db 137 GGCAGTGCAGGAGTAGTGTTCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 196
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CP 1870 GGCAGTGCAGGAGTAGTGTTCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 1811
Db 197 CTCTCTCACAAG 256
|||||
CP 1810 CTCTCTCACAAG 1751
Db 257 TAACCTTAATCTGGAATGCAATAGAGATGCTTAACCTTAATCTGGAATCTGATCTGT 316
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CP 1750 TAACCTTAATCTGGAATGCAATAGAGATGCTTAACCTTAATCTGGAATCTGATCTGT 1691
Db 317 ACTCAAG 376
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CP 1690 ACTCAAG 1631
Db 377 CTAAATTTGGCCACCAAG 436
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CP 1630 CTAAATTTGGCCACCAAG 1571
Db 437 ATGAGACTGACACAGTAAGATCTGAGAGTATAC 474
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CP 1570 ATGAGACTGACACAGTAAGATCTGAGAGTATAC 1533

RESULT 2
LOCUS W69774 450 bp mRNA EST 16-OCT-1996
DEFINITION z48906.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone
ACCESSION W69774
NID g1379032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 450)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marz, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 580 Std Error: 0.00
Seq primer: mob. RECA+ER
High quality sequence stop: 380.
Location/Qualifiers
1. 450
/organism="Homo sapiens"
/note="Organ: heart; Vector: pTZ3 (Pharmacia) modified
polylinker; Site_1: Not I; Site_2: Eco RI;
strand cDNA was primed with a Not I - oligo(dT) primer."
TGTTACCAATCTGAGTGGGAGGCGCCGACATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBH19W."

FEATURES

source

Query Match 21.5% Score 428; DB 21; Length 450;
Best Local Similarity 98.7% Pred. No. 0.00e+00;
Matches 442; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

BASE COUNT 130 a 96 c 134 g 87 t 3 others

ORIGIN

Db 3 AGTCAAGGTTTATCATGATCCCAAGAGCCAGAGAGACTTTAGACATTAATAGGATA 62
|||||
CP 1990 AGTCAAGGTTTATCATGATCCCAAGAGCCAGAGAGACTTTAGACATTAATAGGATA 1931
Db 63 AAGCAAGGCCACAGGCTCCAGCTCCTGATGCCAGATGTCGGCAGATCCGGGACAG 122
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CP 1930 AAGCAAGGCCACAGGCTCCAGCTCCTGATGCCAGATGTCGGCAGATCCGGGACAG 1871
Db 123 GGCAGTGCAGGAGTAGTGTTCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 182
|||||
CP 1870 GGCAGTGCAGGAGTAGTGTTCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 1811
Db 183 -TTCTTCAAAAG 241
|||||
CP 1810 CTCTCTCACAAG 1751
Db 242 TAACCTTAATCTGGAATGCAATAGAGATGCTTAACCTTAATCTGGAATCTGATCTGT 301
|||||
CP 1750 TAACCTTAATCTGGAATGCAATAGAGATGCTTAACCTTAATCTGGAATCTGATCTGT 1691
Db 302 AGTCAAG 361
|||||
CP 1690 AGTCAAG 1631
Db 362 GCTAAATTTGGCCACCAAG 421
|||||
CP 1631 GCTAAATTTGGCCACCAAG 1571
Db 422 AATGAGACTGACACAGTAAGATCTG 449
|||||
CP 1571 AATGAGACTGACACAGTAAGATCTG 1544

RESULT	3	AA687725	396 bp	MRNA	EST	11-DEC-1997
LOCUS		AA687725				
DEFINITION		nv0806.1	NCI-CGAP_P122	Homo sapiens	CDNA clone	IMAGE:1219594,
ACCESSION		AA687725				
NID		92874631				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
AUTHORS		Primates; Catarrhini; Homnidae; Homo.				
TITLE		1 (bases 1 to 396)				
JOURNAL		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
COMMENT		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
		Tumor Gene Index				
		Unpublished (1997)				
		Contact: Robert Strausberg, Ph.D.				
		Tel: (301) 496-1550				
		Email: Robert.Strausberg@nih.gov				
		Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.				
		Emmert-Buck, M.D., Ph.D.				
		CDNA Library Preparation: M. Bento Soares, Ph.D.				
		CDNA Library Arrayed by: Greg Lennon, Ph.D.				
		DNA sequencing by: Washington University Genome Sequencing Center				
		clone distribution: NCI-CGAP clone distribution information can be				
		found through the I.M.A.G.E. Consortium/MLN at:				
		www.bio.llnl.gov/bdhp/image/image.html				
FEATURES						
SOURCE						
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		High quality sequence stop: 331.				
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		1..396				
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		/note="Organ: prostate; Vector: pT713D-Pac (Pharmacia)				
		with a modified polylinker: 1st strand cDNA was prepared				
		from normal prostate bulk tissue, and was then primed with				
		a Not I - oligo(dT) primer. Double-stranded cDNA was				
		ligated to Eco RI adapters (Pharmacia), digested with Not				
		I and cloned into the Not I and Eco RI sites of the				
		modified pT713 vector. Library is normalized, and was				
		constructed by Bento Soares and M. Fatima Bonaldo."				
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		/clone="IMAGE:1219594"				
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ORIGIN						
		Query Match				
		Best Local Similarity 99.2%; Score 389; DB 11; Length 396;				
		Matches 392; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
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Cp	1930	AAGCAAGGCCACAGAGCTTCAGCTGATGCCCGCAGATGTTGCGAGAGATCCGGGACAG	1871			
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Cp	1870	GCGAGTCGAGCAGTAGTTTTCATCTCTCCACTCAGAGAGAGAGACGAGGGGGCAGAGC	1811			
Db	182	ATTCTTCAACAAAGAGATGACTTCTTAGCGCTGCTCGAAGACACCACTCTCCTTACC	241			
Cp	1810	ATTCTTCAACAAAGAGATGACTTCTTAGCGCTGCTCGAAGACACCACTCTCCTTACC	1751			
Db	242	TAACTTATATCTGAGATCAATAGAGATGGCTACTACTTATGATTCTGTGATCTGCT	301			

Cp	1750	TACCCCTAATGTGGAAATGCATATAGAGAAGGCTTAACCTATTATAGATTCGTGGATCCTCGT	1691
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Cp	1630	CTAATTTGGCCACCAAGSAGGGGCGAGCATGAT	1596
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DEFINITION	z1259g1.g1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA		
ACCESSION	AA678356		
NID	92658878		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
AUTHORS	Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 373) Haller,D., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Kritzman,D., Kucuba,T., Lacy,M., Le,N., Lennon,G., Marra,N., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Thelings,B., White,Y., Wylie,T., Waterston,R. and Wilson.R. WashU-NCI human EST Project Unpublished (1997)		
TITLE	contact: Wilson R		
JOURNAL	Washington University School of Medicine		
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL : con'tac' t' IMGE Consortium (info@image.llnl.gov) for further information. Sense primer: -40ml3 fwd. Ex from Amersham High quality sequence stop: 365. Location/Qualifiers 1..373 /organism="Homo sapiens" /note="Organ: Liver and Spleen; Vector: pTZ19D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: EcoRI This is a subtracted version of the original non-purified liver spleen INFLS library. 1st strand cDNA was purified with a Pac I - oligo(dT) primer [5]. ACTGCAAGATTAAATTAAGAGATCTTTTTTTTTTTTTTTT double-stranded cDNA was ligated to Eco RI sites (Pharmacia), digested with Pac I and cloned into and Eco RI sites of the modified pTZ19 vector. went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldi. /db_xref="taxon:9606" /clone="431856" /clone_id="Soares fetal liver spleen INFLS S1" /sex="male" /dev_stage="20 week-post conception fetus" /_lab_host="DH10B (ampicillin resistant)"		
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Query Match	18.0%; Score 358; DB 11; Length 373;		
Best Local Similarity	99.2%; Pred. No. 0.00e+00;		
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Cp	1990	AGTCAGAGTTAATCATGATCCAAAGGCCAGACAGACTTAGACATAATAGCAATA	1991
Db	66	AAGCAAGGCCAACAGGCTCCAGCTCCGATGCCAGATATGTTGGCAGAGATCCGGGGACAG	125

CP	1930	AAGCAGAGGCCACAGGCTCCAGCTCCTATGCGCCAGAGTTCGGCAGAGATCCGGGGACAG	1871
Db	126	GGCAGTGCAGGCAGTAGTTCCTTCATCTTCACCTACAGAGAGAGACGAGGGGCGCAGACC	185
CP	1870	GGCAGTGCAGGCAGTAGTTCCTTCATCTTCACCTACAGAGAGAGACGAGGGGCGCAGACC	1811
Db	186	-TTCTTCACAAAGAGAAATGATCTTCTAGGCTGGGCTCGAAGACACCAGTCTCCCTACCC	244
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Db	245	TAAACCTAATCTGGAATGCAATAGAAATGGCTAACTATTAGATTGTGGTGAATCCTGGT	304
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Db	305	AGTCAGAGAGAGAGGCTCAGAAAAGGGGCTTGGTGGAGCTGTGCACACACAGATGACATGG	364
CP	1690	AGTCAGAGAGAGAGGCTCAGAAAAGGGGCTTGGTGGAGCTGTGCACACACAGATGACATGG	1631
Db	365	CTAATATGT 373	
CP	1630	CTAATATGT 1622	
RESULT	5		
LOCUS	W69813	436 bp	mRNA
DEFINITION	cd48806.r1 Soares fetal heart NBH19W	Homo sapiens	CDNA clone
ACCESSION	W69813		
NID	91379141		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 436)		
AUTHORS	Hillier,L., Clark,N., Dubnue,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kubea,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treviskins,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.		
TITLE	The Washu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAG Consortium (info@image.llnl.gov) for further information. Insert length: 580 Std Error: 0.00 Seq primer: mob. REGA+ET High quality sequence stop: 327. Location/Qualifiers 1..436 /organism="Homo sapiens" /note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer TGTTCACATCTGAAGTGGAGCGCGCCGACATCTTTTCTTTTCTTTT 3'." double-stranded CDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Boudado. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."		
FEATURES			
source			
	/db_xref="taxon:9606"		
	/clone="343930"		

Query Match	17.7%	Score 352	DB 21	Length 436
Best Local Similarity	98.0%	Pred. No. 0.00e+00		
Matches 384	Conservative	0	Mismatches 3	Indels 5
				Gaps 5
BASE COUNT	88 a	130 c	104 g	113 t
ORIGIN				1 others
Query Match	17.7%	Score 352	DB 21	Length 436
Best Local Similarity	98.0%	Pred. No. 0.00e+00		
Matches 384	Conservative	0	Mismatches 3	Indels 5
				Gaps 5
BASE COUNT	88 a	130 c	104 g	113 t
ORIGIN				1 others

REFERENCE	LOCUS	8	AA050083	465 bp	mRNA	EST	09-SEP-1996
AUTHORS	DEFINITION		U0108405_r1	Soares mouse embryo	NbMK13.5	14.5	Mus musculus cDNA
TITLE	ACCESSION		AA050083	clone 47497 5',	mRNA sequence.		
JOURNAL	NID		91529753	EST.			
COMMENT	KEYWORDS		house mouse.				
	SOURCE		Mus musculus				
	ORGANISM		Eukaryote; mitochondria	eukaryotes; Metazoa; Chordata;			
			Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae				
Mus.							
1 (bases 1 to 465)							
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuqu							
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,							
Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,							
Wheising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and							
Waterston,R.							
The WashU-HM1 Mouse EST Project							
Unpublished (1996)							

Contact: Maria M/Mouse EST Project
 Mashu-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1600
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information
 MGI:286241
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence scop: 431.
 Location/Qualifiers
 1..465

```

/organism="Mus musculus"
/strain="C57Bl/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCCGCCGGAATTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Watsu
State Univ., from 2 } double-stranded cDNA was ligated
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fátima Ronaldo."
/db_xref="taxon:10090"
/clone="475497"
/clone_1lb="Soares mouse embryo NDME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
<1.->465
100 a 147 c 128 g 90 t

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Query Match	11.7%	Score 232;	DB 21;	Length 465;
Best Local Similarity	81.5%	Pred. No. 0.00e+00;		
Matches 313;	Conservative	0;	Mismatches 69;	Indels 2; Gaps
Db	84	CTATGATCCTGCTACTGCTGCTGTGTGTGGCTGCCACTTGGAGCAGAAACTCCTT	143	
QY	245	CTGATGTTGGTGGCTGCTGCTGCCGCGTCGCTCCCTCTCTGCGACCCGAGAACCCCTT	304	
Db	144	GCCACAGAGAACAAGTTGTGAACAGGTATACCCAGGCCAGAAAGATGCGAGGCTAT	203	
QY	305	CCCCACAAAGCCGACATCAATGAACAGCTGTCTCTCAGGCCAGAGAGAAAGTCCAGGCTAT	364	
Db	204	CCCGCTTGCAAGCGCTGCTATCCAGCACTGGGCTCTCGACCTCAGT-TAAGCAGGGCG	262	

[illegible][illegible]

REFERENCE	1
(Pages 1 to 189)	
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kizman, D., Kucaba, T., Lacey, M., Le, N., Lenono, G., Mair, M., Martin, J., Moore, B., Schellenberg, R., Stepien, G., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.	
Washington NCI human EST Project	
Unpublished (1997)	

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 182.

```

FEATURES
Source
Location/Qualifiers
1..189
/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia), ligated to Eco RI sites with a modified polylinker; Site_1: Pac I; Site_2: Eco RI."
This is a subcloned version of the original Soares liver spleen INFRS library. 1st strand cDNA was prepared from total RNA isolated from liver spleen INFRS library.
with a Pac I - oligo(dT) primer [5', AACGCAACATTTAATTAAAGACTCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the BamHI site of the modified pT7T3 vector. Library constructed by Bento Soares and M.Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="433223"
/clone_1b="Soares fetal liver spleen INFRS SI"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"

```

Query Match 9.18; Score 181; DB 11; Length 189;

OY	2	AAGTCGAAGGTTTAATCATGTATGCATCCAGAGGCCACAGAGACTTITAGACAAATRAATAGMAT	61
Db	61	AAAGCAAGCCCCACAGGGCTTCAGCTCCTCATATGCCAGATGTTGGCGAGATCCGGGACA	120
OY	62	AAACCAAGGCCCCACAGGCTTCAGCTCCTGATGCCAGATGTTGGCGAGAATCCGGGACA	121
Db	121	GGCGAGTGCGAGCGATAGTATTTCATCCCTCACATGAGAGAGAACAGCAGGGG	173
OY	122	GCGCAGTGCGAGCGATAGTATTTCATCCCTCACATGAGAGAGAGAAC- CGAGGGG	173
RESULT	12		
LOCUS	AA694259	474 bp	mRNA
DEFINITION	Z13J11.1.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone 432405 3', mRNA sequence.	EST	16-DEC-1997
ACCESSION	AA694259		
NID	92695197		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 474) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Giesel,G., Jost,S. Kritzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Maria,M., Martin,J., Moore,B., Schellenberg,K., Stepecoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.		
TITLE	WashU-NCI human EST Project		
JOURNAL	Unpublished (1997)		
COMMENT			

FEATURES

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (imageimage.lln.gov) for further information.
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 451.
Location/Qualifiers

```

source
1. .474
/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia with a modified polylinker; Site_1: Pac I; Site_2: Eco RI). This is a subtracted version of the original Soares fetal liver spleen mFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACGCAAGACATTAATTAACATCTTTTCTTTTCTTTTCTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
/db_xref="GDB:1332174"
/db_xref="taxon:9606"
/clone_1id="432405"
/clone_1lb="Soares fetal liver spleen mFLS S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
134 a 100 c 137 g 103 t

```

Query Match	8.0%	Score 160;	DB 11;	Length 474;
Best Local Similarity	97.7%	Pred. No. 2,258-258;		
Matches	169;	Conservative	0;	Mismatches 3; Indels 1; Gaps 1

Db	16	AAGTCGAAGGTTTATATCATGATCCAAAGAGCCAGAGACTTTTGGACAAATATAGCAAT	75
OY	2	AAGTCGAAGGTTTATATCATGATCCAAAGAGCCAGAGACTTTTGGACAAATATAGCAAT	61
Db	76	AAAGCAAGGCCACAGGCTCCAGCTCTGTGATGCCCAATATGTTGGCGAGGATCCGGGGACA	135

OY |||||
62 MAMGCAAGGCCACAGSGTCCAGTCCTGTATGCCAGAAATTTCGGCAGGATCCGGGGACA 127
Dd GGCAGTAGCGAGCAGCAATAGTTTTCATCCTCCTCACCTCAGAGGAGAGACGAGG 188
OY 122 GGCACTAGCAGGCACTAATTTTTCATCCTCCTCATCCACGAGGGAGAG- CGAGGG 173

RESULT	13								
LOCUS	AA984036	350 bp	mrna	EST	07-JUL-1998				
DEFINITION	OQ02402.s1 NCI_CGAP_Lus	Homo sapiens	CDNA clone	IMAGE:1585179	3'				
ACCESSION	AA984036								
NID	G3162561								
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;								
AUTHORS	Primates; Catarrhini; Homiidae; Homo.								
TITLE	1 (Bases 1 to 350)								
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .								
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),								
	Tumor Gene Index								
	unpublished (1997)								

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/dbrp/image/image.html

FEATURES

Insert Length:	762	Std Error:	0.00
Seq primer:	-40m13 fwd.	ET from	Amersham
High quality	sequence stop:	284.	
Location/Qualifiers			

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source
1. 350
/organism="Homo sapiens"
/note="Organ: Lung; Vector: pT73D-Pac (Pharmacia) with
modified polylinker; 1st strand cDNA was prepared by
neuroendocrine lung carcinoma, and was then primed with
Not I - oligo(dT) primer. Double-stranded cDNA was
cloned into the Not I and Eco RI sites of the
pT73 vector. Library is normalized. Library
constructed by Bento Soares and M. Fatima Toledo"
/db_xref="taxon:9606"
/clone="IMAGE:158519"
/clone_1lb="NCI CGAP Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
100 a 81 c 96 g 73 t

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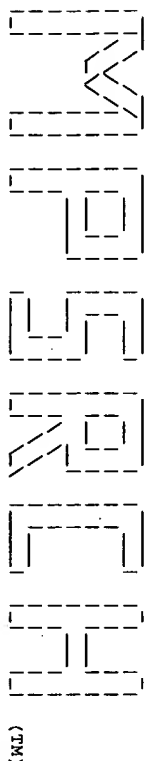
Query Match	7.9%	Score 158:	DB 15:	Length 350:
Best Local Similarity	97.18:	Pred. No. 3.06e-254:		
Matches 168:	Conservative 0:	Mismatches 4:	Indels 1:	Gaps 1:
Db	6	AACTCAAAGGTTTAATCATGATTCACAGAGCCCGCAGAGAGACTTTAGGACATATATAGTAAT	67	
QY	2	AAATCAAAGGTTTAATCATGATTCACAGAGCCCGCAGAGAGACTTTAGGACATATATAGTAAT	7	
Db	66	AAAGCAAGGCCACACAGGCAACAGCTCTATGATGCCCGCAGATGTTGCGCAGATTCGCGCGG	73	
QY	62	AAAGCAAGGCCACACAGGCTCCAGCTCTGTCGCCGAGATGTTGCGCAGATTCGCGCGG	73	
Db	126	GGGCATTCGACAGCAGTAGTATTTCCATCCCTCCACTCAGAGAGGACACGAGCGG	178	

RESULT	14	450 bp	EST	16-OCT-1996
LOCUS	W69774			
DEFINITION	z4d8g06.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone			
ACCESSION	343930.3	3'	mRNA sequence.	
NID	W69774			
KEYWORDS	g1379032			
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;			
	Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 450)			
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Merri, A., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevastis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.			
TITLE	The WashU-Merck EST Project			
JOURNAL	Unpublished (1995)			
COMMENT	<p>Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu</p> <p>This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.lml.gov) for further information. Insert Length: 580 Std Error: 0.00 Seq primer: mob.REGA+ET</p> <p>High quality sequence stop: 380.</p>			
FEATURES	<p>Location/Qualifiers</p> <p>1..450</p>			
SOURCE	<p>/organism="Homo sapiens" /Note="Organ: heart; Vector: p7T3D (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5 TGTTCACATCTGAGTGGAGCGGCGCCGATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHH19W." /db_xref="taxon:9606" /clone="343930" /clone_1lb="Soares fetal heart NBHH19W" /sex="unknown" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" complement(<1..>450)</p>			
BASE COUNT	130 a	96 c	134 g	87 t 3 others
ORIGIN	<p>mrna</p>			
Query Match	7.9%	Score 158:	DB 21:	Length 450:
Best Local Similarity	97.1%	Pred. No. 3.06e-254:		
Matches 168:	Conservative 0:	Mismatches 4:	Indels 1:	Gaps 1:
Db	2	AAAGTCAAGGCTTAAATCATGATCCAGAGCCCGAGAGAGACTTTAGGACATATAGGAAT	61	
Oy	2	AAAGTCAAGGCTTAAATCATGATCCAGAGCCCGAGAGAGACTTTAGGACATATAGGAAT	61	
Db	62	AAAGCAAGGCCACAGAGCTCCAGCTCTGTATGCCAGATTTGGGAGAGATCCGGGACA	121	
Oy	62	AAAGCAAGGCCACAGAGCTCCAGCTCTGTATGCCAGATTTGGGAGAGATCCGGGACA	121	
Db	122	GGGCAAGTGCAGGCGATGTTGTTTCATCTCTCCACTCAGAGAGAGACGAGGGG	174	

[illegible]

```
Qy      305  ||||| | | | ||||| ||||| | | | ||||| |
          CCCACAGAAAGCCGACTCATGAACAGCTGCTCCAGGCCAGGAGAGTGCCAGGCTGAT 364
Db      205  CCCGCTTGCAAGGCTGCTACCAAGCAGCTGGGCTCCTGCACCTCCAGT--TAAGCAGGGCG 263
          ||| | ||| ||||| ||||| ||||| ||||| ||| ||||| ||
Qy      365  CCCACCTGCAGTGCTGCTACCAAGCAGCTGATTCCTGCACTTAAGCAGGCCA 424
          ||||| ||||| | | | ||||| ||||| ||||| ||||| ||
Db      264  CTGCCCTTAGAGAGTCTGCCATGTCTGCAGACTGCTAGAGGACAGACACTCAG 323
          ||||| ||||| | | | ||||| ||||| ||||| ||||| ||
Qy      425  CTGCCCTCAGAGAGGCTTCGGTCCCTGCTGACTGCTGAGGACAGCAGCACTCAG 484
          ||||| ||||| | | | ||||| ||||| ||||| ||||| ||
Db      324  AACAGCTCTGTATAGACTGCAGTGCCA 352
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Qy      485  AACAGCTCTGTATAGCTGCATGTGCCA 513
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

Search completed: Fri Mar 12 04:34:58 1999
Job time : 4622 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

Mparch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:13:58 1999; Maspar time 14.47 Seconds

Tabular output not generated. 447.378 Million cell updates/sec

Title: >US-08-866-354-38
Description: (1-400) from US08866354.pep
Perfect Score: 3033
Sequence: 1 MVRPLNRPPLPPVYVLMILL.....PWVSLSCPLILLSLW 400

Scoring table:
PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a.geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.299; Variance 146.727; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3029	99.9	400	28	W37463 Human Ret ligand RetL	7.97e-287
2	2378	78.4	315	28	W37462 Human Ret ligand RetL	1.80e-221
3	2356	77.7	397	28	W37461 Mouse Ret ligand RetL	2.89e-221
4	2074	68.4	346	28	W37459 Mouse Ret ligand RetL	5.03e-191
5	717	23.6	460	28	W37459 Human Ret ligand RetL	1.74e-56
6	701	23.1	464	28	W37460 Human Ret ligand RetL	6.25e-55
7	686	22.6	465	28	W35333 Human glial cell line	1.79e-53
8	678	22.4	468	28	W37457 Rat Ret ligand RetL	1.07e-52
9	678	22.4	468	28	W27337 Rat glial cell line-d	1.07e-52
10	678	22.4	468	28	W35334 Rat glial cell line-d	1.07e-52
11	532	17.5	346	28	W37458 Human Ret ligand RetL	1.31e-38
12	113	3.7	1015	27	W25171 Human insulinom-asso	1.09e+00
13	113	3.7	1015	27	W35345 Human protein tyrosin	1.09e+00
14	113	3.7	1015	27	W18092 Type I diabetes-asso	1.09e+00
15	110	3.6	969	24	W25170 Human insulinom-asso	1.83e+00
16	106	3.5	1012	27	W35296 Macaque islet cell an	3.64e+00
17	101	3.3	102	13	R70793 Gro-beta/MIP-2-alpha	8.48e+00
18	101	3.3	107	4	R23034 Human Gro beta cytol	8.48e+00

19	101	3.3	107	4	R20529 Human macrophage IntL	6.4e+01
20	101	3.3	107	4	R20589 Human macrophage IntL	6.4e+01
21	101	3.3	505	10	R55369 Human Activin recepto	1.95e+01
22	98	3.2	228	19	R98742 Tazartene induced ve	1.95e+01
23	96	3.2	599	4	R21690 Prostaglandin endoper	1.95e+01
24	96	3.2	638	25	W32098 Miniature swine retro	1.95e+01
25	96	3.2	1481	19	W03740 rchd528 gene product	1.95e+01
26	94	3.1	505	10	R55373 Mouse Activin recepto	2.7e+01
27	94	3.1	505	13	R70240 Serine/threonine kina	2.7e+01
28	91	3.0	113	27	W35449 Human chemokine alpha	4.40e+01
29	90	3.0	223	29	W43407 Human acylcoenzymase A	5.17e+01
30	90	3.0	384	24	W23278 Bordetella pertussis	4.40e+01
31	90	3.0	458	19	R98744 h-IGFBP-4	5.17e+01
32	87	2.9	322	4	R23209 Sequence of insulin-1	8.34e+01
33	87	2.9	324	4	R21833 Arabidopsis violaxant	8.34e+01
34	87	2.9	462	22	W05876 Mullerian inhibiting	6.07e+01
35	89	2.9	501	18	W03760 MISRA/MISR2B	6.07e+01
36	89	2.9	505	8	R41921 Canine herpesvirus q1	6.07e+01
37	89	2.9	522	26	W23000 A. niger strain M-62	8.34e+01
38	87	2.9	670	19	R94370 Human protocadherin-4	8.34e+01
39	87	2.9	1026	11	R58906 Protocadherin clone 4	8.34e+01
40	87	2.9	1026	17	R87146 Inositol-1,4,5-tripho	8.34e+01
41	87	2.9	1096	20	W01596 Alternatively spliced	8.34e+01
42	87	2.9	1203	17	R87152 Product of alternativ	8.34e+01
43	87	2.9	1203	17	R58911 Chicken cytotactin	7.11e+01
44	88	2.9	1810	16	R94563 G-CSF deriv. without	9.76e+01
45	86	2.8	181	3	R13369	

ALIGNMENTS

RESULT 1
ID W37463 standard; Protein: 400 AA.
AC W37463:
DT 21-MAY-1998 (first entry)
DE Human Ret ligand RetL3.
KW Ret ligand; RetL; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neuron disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN W09744356-82.
PD 27-NOV-1997.
PE 07-MAY-1997: U07726.
PR 10-APR-1997: US-017427.
PR 08-MAY-1996: US-017427.
PR 07-JUN-1996: US-019300.
PR 16-JUL-1996: US-021859.
PA (BIO) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
DR WPI: 98-018431/02.
DR N-PSDB: V00251.
PT New nucleic acid encoding ret receptor ligands and related proteins;
PT - vectors, transformed cells and antibodies; used for promoting cell
PT growth and improving survival of injured cells, especially renal cell
PT nerve cells
PS Claim 2: Page 85-86; 113pp: English.
CC This amino acid sequence comprises human Ret ligand (Ret) RetL3,
CC deduced from cDNA clones (see V00251) isolated from a adult human
CC and spinal cord libraries. Rat and human RetL, human RetL2 and
CC mouse RetL sequences (see W37457-62) are also claimed. Human
CC RetL3 is 34.3% identical to human RetL. 34.9% identical to human
CC RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key
CC component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret domain
CC and/or autophosphorylation of the Ret tyrosine kinase
CC Vectors containing retL DNA and prokaryotic or eukaryotic host
CC cells transformed or transfected with these vectors are claimed,
CC well as a method for production of RetL3, its soluble variants and

CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 400 AA:

Query Match 99.9%; Score 3029; DB 28; Length 400;
 Best Local Similarity 99.8%; Pred. No. 7,976-287;
 Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mvrplnrplrpvlml11111ppsp1laagdp1pcesrlmsclqarrkcgadpcsa 60
 1 mvrplnrplrpvlml11111ppsp1laagdp1pcesrlmsclqarrkcgadpcsa 60
 Db 61 yhlldscststipjseepsvadcleaag1lmsl1gcmchrnkqvacldiytv 120
 61 yhlldscststipjseepsvadcleaag1lmsl1gcmchrnkqvacldiytv 120
 Db 121 hraslgyvelvsvpedvtstkpm1sklm1kpsddldlckfamctlnkdcdrlx 180
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 Db 181 aygeacspqhcgrhvc1rlq1ltfekaephagq11lpcapnd1gcsgrrrntlapna 240
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 Db 181 aygeacspqhcgrhvc1rlq1ltfekaephagq11lpcapnd1gcsgrrrntlapna 240
 181 aygeacspqhcgrhvc1rlq1ltfekaephagq11lpcapnd1gcsgrrrntlapna 240
 Db 241 lrpvpnclelrrlcfed1crslvd1qthchpmd1lgtcetegrc1ray1lgtam 300
 241 lrpvpnclelrrlcfed1crslvd1qthchpmd1lgtcetegrc1ray1lgtam 300
 Db 301 tnfnsnvtswalstcrgsgnlgcecm1egfshmpclleaakmrfhsq1fsqdw 360
 301 tnfnsnvtswalstcrgsgnlgcecm1egfshmpclleaakmrfhsq1fsqdw 360
 Db 361 phrtfvmahqneapv1rpqwp1sfsc1p11111slw 400
 361 phrtfvmahqneapv1rpqwp1sfsc1p11111slw 400
 Db 361 phrtfvmahqneapv1rpqwp1sfsc1p11111slw 400
 361 phrtfvmahqneapv1rpqwp1sfsc1p11111slw 400

RESULT 2
 ID W37462 standard; Protein: 315 AA.
 AC W37462;

DE Human Ret ligand RetL3 partial sequence.
 KW Ret ligand; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN MO9744356-A2.
 PD 27-MAY-1997;
 PE 07-MAY-1997; 007726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00250.

PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2; Page 81-82; 113pp: English.
 CC This amino acid sequence comprises a human Ret ligand (RetL3)
 CC partial polypeptide sequence, deduced from a partial clone (see
 CC V00250) isolated from a human adult heart cDNA library; a
 CC full-length RetL3 sequence (see W37463) is also claimed, as well
 CC as rat and human RetL1, human RetL2 and mouse RetL3 sequences
 CC (see W37455-61). Ret ligand is a key component of the Ret
 CC signalling pathway that specifically interacts with Ret receptor
 CC protein, triggering Ret dimerisation and/or autophosphorylation of
 CC the Ret tyrosine kinase domain. Vectors containing retL3 DNA and
 CC prokaryotic or eukaryotic host cells transformed or transfected
 CC with these vectors are claimed, as well as a method for production
 CC of RetL3, its soluble variants and fusion proteins with a toxin,
 CC imageable compound or radionuclide. RetL3, optionally when
 CC expressed from vectors in vivo, is used to promote growth of new
 CC tissue and survival of damaged tissue, particularly kidney or
 CC neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 315 AA:

Query Match 78.4%; Score 2378; DB 28; Length 315;
 Best Local Similarity 99.0%; Pred. No. 1,806-221;
 Matches 308; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 5 tpg1lmsl1gcmchrnkqvacldiytvhras1gnyeldivpedvtstkpm1 64
 5 tpg1lmsl1gcmchrnkqvacldiytvhras1gnyeldivpedvtstkpm1 64
 Db 90 aqolrnsllgcmchrnkqvacldiytvhras1gnyeldivpedvtstkpm1 149
 90 aqolrnsllgcmchrnkqvacldiytvhras1gnyeldivpedvtstkpm1 149
 Db 65 sklm1kpsddldlckfamctlnkdcdrlxaygeacspqhcgrhvc1rlq1ltfeka 124
 65 sklm1kpsddldlckfamctlnkdcdrlxaygeacspqhcgrhvc1rlq1ltfeka 124
 Db 150 sklm1kpsddldlckfamctlnkdcdrlxaygeacspqhcgrhvc1rlq1ltfeka 209
 150 sklm1kpsddldlckfamctlnkdcdrlxaygeacspqhcgrhvc1rlq1ltfeka 209
 Db 125 phag11lpcapnd1gcsgrrrntlapna1lprvanclelrrlcfed1crslvd1q 184
 125 phag11lpcapnd1gcsgrrrntlapna1lprvanclelrrlcfed1crslvd1q 184
 Db 210 phaogllcpapndrccgrrrrntlapna1lprvanclelrrlcfed1crslvd1q 269
 210 phaogllcpapndrccgrrrrntlapna1lprvanclelrrlcfed1crslvd1q 269
 Db 185 tchpmd1lgtcetegrc1ray1lgtamt1fnvntswalstcrgsgnlgcecm 244
 185 tchpmd1lgtcetegrc1ray1lgtamt1fnvntswalstcrgsgnlgcecm 244
 Db 270 tchpmd1lgtcetegrc1ray1lgtamt1fnvntswalstcrgsgnlgcecm 320
 270 tchpmd1lgtcetegrc1ray1lgtamt1fnvntswalstcrgsgnlgcecm 320
 Db 245 mlegfshmpclleaakmrfhsq1fsqdwphrtfvmahqneapv1rpqwp1sfsc 300
 245 mlegfshmpclleaakmrfhsq1fsqdwphrtfvmahqneapv1rpqwp1sfsc 300
 Db 330 mlegfshmpclleaakmrfhsq1fsqdwphrtfvmahqneapv1rpqwp1sfsc 360
 330 mlegfshmpclleaakmrfhsq1fsqdwphrtfvmahqneapv1rpqwp1sfsc 360
 Db 305 tlp1111slw 315
 305 tlp1111slw 315
 Db 390 tlp1111slw 400
 390 tlp1111slw 400

RESULT 3
 ID W37461 standard; Protein: 397 AA.
 AC W37461;

DE Mouse Ret ligand RetL3.
 KW Mouse Ret ligand RetL3.
 KW Ret ligand; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;

AC W37459; (first entry)
 DT 21-MAY-1998
 DE Human Ret ligand RetL1.
 KW Ret ligand; RetL1; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN WO9744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR MPI: 98-018431/02.
 DR N-PSDB: V00247.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT -vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 64-66; 113pp; English.
 CC This amino acid sequence comprises human Ret ligand (RetL1) RetL1,
 CC deduced from cDNA clones (see V00247) isolated from a human
 CC foetal kidney. Rat RetL1 and mouse and human RetL2 and RetL3
 CC sequences (see W37457 and W37460-63) are also claimed. The
 CC human RetL1 sequence is 93.3% identical to that of rat. Ret ligand
 CC is a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor, triggering Ret dimerisation and/or
 CC autophosphorylation of the Ret tyrosine kinase domain. Vectors
 CC containing retL1 DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of RetL1, its soluble variants and fusion
 CC proteins with a toxin, imageable compound or radionuclide. RetL1,
 CC optionally when expressed from vectors in vivo, is used to promote
 CC growth of new tissue and survival of damaged tissue, particularly
 CC kidney or neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 460 AA:
 Query Match 23.6%; Score 717; DB 28; Length 460;
 Best Local Similarity 36.5%; Pred. No. 1,74e-56;
 Matches 125; Conservative 69; Mismatches 129; Indels 19; Gaps 17;
 Db 6 lyfalpldlila-e-vsgdrl-d-cvkaadqclkegcskyrtllrgvagketnfs 61
 Oy 17 LLLLPSPPLAAGPLPTESRLMNSCLQARRCCADPTCSAAYHLLDCTSSISPTLP 76
 Db 62 laasgleekdecraamealjkxslyncrcrgmkckncrlqysamygsld-gndldesp 120
 Oy 77 -SEEPSVPADCLEAAOQLRRSSSLIGCMCHRRMKNQVACLDIYTVHARSGLVETDVP 135
 Db 121 ye-pvnarlsladfrvvpflsvehlipkgncldaakacnldldckkyrsayltcctsvsn 179
 Oy 136 YEDTVTSKPKM-KLSK-LVMTK-PPSDCLCFKAMLCITWDKDRLRKAAGCAES-G-PH 190
 Db 180 dvenrrtkchakalrqfdkypakhsygmifsc--rdlaacterrrtqtlvpvcyeeekpn 237
 Oy 191 --CORHVCRLQTLTFEKAEPHQAQGLICPCAPRNDRCGERRRNTIAPCALPVA-PN 247

Db 238 cnlgscktnyrcrcladffncgpearsvscikenyadcllasyllgtvmtpnvyl 297
 Oy 248 CLELRRLCRSDPLCRRLVDFQTHCPMDI-LGTATEQ-SNCLRAYLGLISTAMTPNRA 305
 Db 298 dssalsvapwcdscnsgndleclklfnlfkntclkaqla 339
 Oy 306 SNNVTSVALSCRCRSGNLOEBCMELEGFSSNPLCTEAIAA 347
 RESULT 6
 ID W37460 standard; Protein: 464 AA.
 AC W37460;
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL2.
 KW Ret ligand; RetL2; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN WO9744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR MPI: 98-018431/02.
 DR N-PSDB: V00248.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT -vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 69-70; 113pp; English.
 CC This amino acid sequence comprises human Ret ligand (RetL2) RetL2,
 CC deduced from a cDNA clone (see V00248) isolated from a human foetal
 CC liver library. Rat and human RetL1, and human and mouse RetL3
 CC sequences (see W37457-59 and W37461-63) are also claimed. Human
 CC RetL2 is 49.1% identical to human RetL1 protein. RetL2 is a
 CC key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing retL2 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL2, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL2, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 464 AA:
 Query Match 23.1%; Score 701; DB 28; Length 464;
 Best Local Similarity 35.7%; Pred. No. 6.25e-55;
 Matches 115; Conservative 87; Mismatches 95; Indels 25; Gaps 18;
 Db 40 cvranelcaesncsryrtllrgclag-rdr-ntmlan--kcgaaalevgsplydcrc 95
 Oy 44 CLQARRCCADPTCSAAYHLLDCTSSISPTLPSEPSVPADCLEAAOQLRRSSSLIGCMC 103

 WISE (TM)

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:16:14 1999; Maspar time 21.09 Seconds

Tabular output not generated. 710.686 Million cell updates/sec

Title: >US-08-866-354-38
 Description: (1-400) from US08866354..pep
 Perfect Score: 3033
 Sequence: 1 MVRPLNRPPLPVLMILL.....PMVPSLFSCTPLILLSLM 400

Scoring table:
 PAM 150
 Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r58
 1:p1r1.2:p1r2.3:p1r3.4:p1r4

Statistics: Mean 45.680; Variance 83.673; scale 0.546

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2356	77.7	397	2	JF0082	GPI-linked receptor - 0.00e+00
2	126	4.2	117	2	S52612	probable membrane pro
3	116	3.8	354	1	XRECO2	adaptive response reg
4	113	3.7	345	2	AS3138	gas1 homolog - human
5	113	3.7	1015	2	JC5263	transmembrane tyrosin
6	113	3.7	1015	2	JC5062	phogorin - human
7	113	3.7	1313	2	JC3038	peptidyl-dipeptidase
8	110	3.6	384	2	S25771	gas1 protein - mouse
9	108	3.6	1309	2	S35484	peptidyl-dipeptidase
10	106	3.5	496	2	A69601	ATP-dependent DNA hel
11	103	3.4	352	1	XVEBOT	adaptive response reg
12	104	3.4	520	2	S36489	I2 protein - human pa
13	101	3.3	107	2	JH0281	macrophage inflamma
14	101	3.3	476	2	I80182	activin type I recept
15	101	3.3	487	2	I80183	activin type I recept
16	100	3.3	2918	2	AS4105	fibrillin-2 precursor
17	97	3.2	61	1	DNPBF	DNA-binding protein -
18	97	3.2	151	2	S33621	ADRI1-2 protein - soy
19	96	3.2	599	2	A36746	prostaglandin-endope
20	97	3.2	607	2	I37560	protein-tyrosine kina
21	98	3.2	2448	2	S35999	pyoverdine synthetase
22	94	3.1	101	2	B28414	growth-regulated prot
23	93	3.1	133	2	JC2202	secretin - mouse

24	95	3.1	175	2	I46199	erythropoietin - dog	1.39e+00
25	95	3.1	188	1	I46083	erythropoietin precu	1.39e+00
26	93	3.1	239	2	S68257	phospholipase C (EC 3	2.54e+00
27	95	3.1	271	2	G64783	ylid protein - Escher	1.39e+00
28	94	3.1	602	2	S69198	prostaglandin G/H syn	1.88e+00
29	93	3.1	631	1	A48346	cell fusion glycoprot	2.54e+00
30	93	3.1	631	1	VGNZPD	cell fusion glycoprot	2.54e+00
31	93	3.1	1049	2	A27079	fibronectin receptor	2.54e+00
32	95	3.1	1053	2	S44250	integrin alpha-5 chain	1.39e+00
33	95	3.1	1102	2	UH0717	guanylate cyclase (EC	1.39e+00
34	94	3.1	1217	2	A45493	phospholipase C-beta	1.88e+00
35	90	3.0	241	2	A64454	hypothetical protein	6.11e+00
36	91	3.0	250	2	S71348	Rieske iron sulfur pr	4.57e+00
37	90	3.0	251	2	S20455	pgc protein - Klebsi	6.11e+00
38	92	3.0	252	2	D32252	gene I protein - Actin	3.41e+00
39	90	3.0	425	2	E71075	probable protein gluta	6.11e+00
40	91	3.0	464	2	A65558	retinoic acid recepto	4.57e+00
41	91	3.0	505	2	I38859	activin A receptor, t	4.57e+00
42	92	3.0	602	2	S39782	cyclooxygenase 1 - ra	3.41e+00
43	91	3.0	651	2	S73558	phosphate transport s	4.57e+00
44	90	3.0	699	2	S27768	RNA-directed DNA poly	6.11e+00
45	90	3.0	1868	2	S48938	hypothetical protein	6.11e+00

ALIGNMENTS

RESULT 1
 ENTRY JE0082 #type complete
 TITLE GPI-linked receptor - mouse
 ALTERNATE_NAMES GFRalpha-3
 ORGANISM Mus musculus #common_name house mouse
 DATE 21-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1998

ACCESSIONS
 REFERENCE JE0082
 #authors Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
 #journal Biochem. Biophys. Res. Commun. (1998) 244:849-853
 #title Molecular cloning and expression analysis of GFRalpha-3
 novel cDNA related to GDNFRalpha and NTRalpha.

#accession JE0082
 #molecule_type mRNA
 #residues 1-397 #label NOM
 #cross-references DBJ:AB008833; NID:92627159; PID:92627159

COMMENT This protein plays a distinct role in cell survival and differentiation.

KEYWORDS
 FEATURE 1-25
 380-397
 92,145,306
 glycoprotein

SUMMARY #length 397 #molecular_weight 44307 #checksum 2962
 Query Match 77.7%; Score 2356; DB 2; Length 397;
 Best Local Similarity 77.9%; Pred. No. 0.00e+00;
 Matches 306; Conservative 53; Mismatches 31; Indels .3; Gaps .

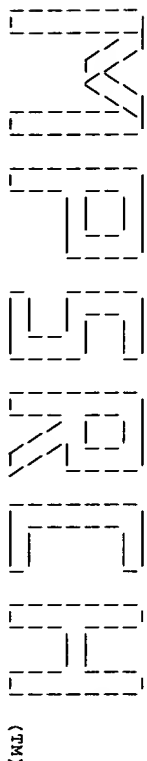
DB	7	PPPLMLLLVLSLW-LPLGANSLATENRFVSCDQARRKCCANPAKRAYOHICST	47
DB	9	PLPVPVLMILLPLPPSLPLAAGDPLPESRLMNSCLQARRKCCADPTCSAAVHHHNSCT	47
DB	66	SLSPPLPERSASADCLFAEDLRNSLIDCCHRMKQACDIDYVHVHNSCT	47
DB	69	SSISTPLPSESPVADCLFAAQDLRNSSLIGCHRMKQACDIDYVHVHNSCT	47
DB	126	YELDVSPYEDVTSTKPMKMNLSKLNMLKPDSDCLKFAMLCTLDKDCRLKAGCAVNSCT	47
DB	129	YELDVSPYEDVTSTKPMKMNLSKLNMLKPDSDCLKFAMLCTLDKDCRLKAGCAVNSCT	47
DB	186	TRCORHCLAOGRFFEFKAESHAQGLLCPACADAGCGERRNTTAPSCALPVSVPNC	245
DB	189	PHCORHCLAOGRFFEFKAESHAQGLLCPACADAGCGERRNTTAPSCALPVSVPNC	245

[illegible]

```

#journal      J. Biol. Chem. (1985) 260:7281-7288
#title        Purification and structure of the intact Ada regulatory
               protein of Escherichia coli K12, O(6)-methylguanine-DNA
               methyltransferase.
#cross-references MUID:85207761
#accession    A22630
##molecule_type DNA
##residues    1-133,'R','I35-354' ##label NAK
##cross-references GB:M10211; NID:g145188; PID:g145189
##experimental_source K12
REFERENCE
#authors      Dempsey, B.; Sedgwick, B.; Robins, P.; Toty, N.; Waterfield,
               M.D.; Lindahl, T.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1985) 82:2688-2692
#title        Active site and complete sequence of the suicidal
               methyltransferase that counters alkylation mutagenesis.
#cross-references MUID:85190562
#accession    A22667
##molecule_type DNA
##residues    1-74,'D','76-78','PR','81-317','V','319-329','S','331-354
               #' ##label DDM
##cross-references GB:M10315; NID:g145190; PID:g145191
##experimental_source strain B/r
REFERENCE
#authors      Nakabeppu, Y.; Sekiguchi, M.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1986) 83:6287-6301
#title        Regulatory mechanisms for induction of synthesis of repair
               enzymes in response to alkylating agents: Ada protein acts
               as a transcriptional regulator.
#cross-references MUID:86313568
#accession    I41114
##status      translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues    1-27' ##label RBS
##cross-references GB:M13828; NID:g145196; PID:g145197
REFERENCE
#authors      Teo, I.; Sedgwick, B.; Kilpatrick, M.W.; McCarthy, T.V.;
               Lindahl, T.
#journal      Cell (1986) 45:315-324
#title        The intracellular signal for induction of resistance to
               alkylating agents in e. coli.
#cross-references MUID:86189944
#accession    I41115
##status      translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues    1-29' ##label RB2
##cross-references GB:M13155; NID:g145198; PID:g145199
COMMENT       This enzyme has an inducible DNA repair system that protects
               against methylating and alkylating agents by transferring the
               alkyl group from O(6)-alkylguanine in DNA to a cysteine residue
               located within the enzyme itself.
GENETICS
#gene         ada
#map_position 48 min
CLASSIFICATION
#superfamily  adaptive response regulatory proteins
#methylated-DNA--protein-cysteine S-methyltransferase
#homology:     methylphosphotriester-DNA methyltransferase
#homology
KEYWORDS       DNA binding; DNA repair; methyltransferase; transcription
               regulation; transferase
FEATURE
7-191          #domain methylphosphotriester-DNA methyltransferase
                #homology #label MPV\
268-348        #domain methylated-DNA--protein-cysteine
                #homology #label MGT\
                #domain methyltransferase homology #label MGR
SUMMARY        #length 354 #molecular-weight 39323 #checksum 7668
Query Match    3.8%; Score 116; DB 1; Length 354;
Best Local Similarity 31.1%; Pred. No. 1,53e+03;
Matches        23; Conservative 17; Mismatches 29; Indels 5; Gaps

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Mar 8 14:17:48 1999; Msearch time 14.56 Seconds
Tabular output not generated. 737.504 Million cell updates/sec

Title: >US-08-866-354-38
Description: (1-400) from US08866354.pep
Perfect Score: 3033
Sequence: 1 MVRPLNRPPLRPVYVLMILL.....PWVSLSTCLPLILLSLW 400

Scoring table:
Gap 11
PAM 150

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot36
1:swissprot

Statistics: Mean 47.118; Variance 74.608; scale 0.632

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	750	24.7	465	1	NRTN_CHICK	3.47e-155
2	746	24.6	469	1	GNDR_CHICK	3.72e-154
3	707	23.3	463	1	GNDR_MOUSE	1.37e-142
4	701	23.1	464	1	NRTN_MOUSE	1.83e-137
5	681	22.5	468	1	GNDR_MOUSE	1.07e-136
6	678	22.4	468	1	GNDR_MOUSE	1.07e-136
7	674	22.2	464	1	GNDR_MOUSE	1.07e-136
8	674	22.2	464	1	GNDR_MOUSE	1.07e-136
9	616	21.8	354	1	ADA_MOUSE	2.00e-04
10	613	21.7	354	1	ADA_MOUSE	2.00e-04
11	613	21.7	354	1	ADA_MOUSE	2.00e-04
12	613	21.7	354	1	ADA_MOUSE	2.00e-04
13	613	21.7	354	1	ADA_MOUSE	2.00e-04
14	613	21.7	354	1	ADA_MOUSE	2.00e-04
15	613	21.7	354	1	ADA_MOUSE	2.00e-04
16	613	21.7	354	1	ADA_MOUSE	2.00e-04
17	613	21.7	354	1	ADA_MOUSE	2.00e-04
18	613	21.7	354	1	ADA_MOUSE	2.00e-04
19	613	21.7	354	1	ADA_MOUSE	2.00e-04
20	613	21.7	354	1	ADA_MOUSE	2.00e-04
21	613	21.7	354	1	ADA_MOUSE	2.00e-04
22	613	21.7	354	1	ADA_MOUSE	2.00e-04
23	613	21.7	354	1	ADA_MOUSE	2.00e-04

24	98	3.2	381	1	DHB2_MOUSE	ESTRADIOL 17 BETA-DEHY	1.53e-01
25	98	3.2	451	1	TBG_ENTHI	TUBULIN GAMMA CHAIN.	1.53e-01
26	96	3.2	2911	1	FBN2_HUMAN	FIBRILLIN 2 PRECURSOR.	3.03e-01
27	94	3.1	101	1	GRO_CRGR	GROWTH REGULATED PROTE	5.96e-01
28	93	3.1	133	1	SECR_MOUSE	SECRETIN PRECURSOR.	8.31e-01
29	95	3.1	175	1	EPO_CANFA	ERYTHROPOIETIN PRECURS	4.26e-01
30	95	3.1	271	1	YLBF_ECOLI	HYPOTHETICAL 29.6 KD P	4.26e-01
31	95	3.1	400	1	PHZF_PSEAR	PROBABLE PHOSPHO-2-DEH	4.26e-01
32	93	3.1	631	1	VGIF_PRODY	FUSION GLYCOPROTEIN PR	8.31e-01
33	95	3.1	692	1	HEXA_ANOGA	HEXAAMERIN 1.1 PRECURS	4.26e-01
34	93	3.1	1049	1	ITAS_HUMAN	FIBRONECTIN RECEPTOR A	8.31e-01
35	95	3.1	1053	1	ITAS_MOUSE	FIBRONECTIN RECEPTOR A	4.26e-01
36	95	3.1	1103	1	CYGD_HUMAN	RETINAL GUANYLYL CYCLA	4.26e-01
37	95	3.1	1109	1	CYGD_CANFA	RETINAL GUANYLYL CYCLA	4.26e-01
38	94	3.1	1441	1	CC12_SCHPO	CELL DIVISION CONTROL	5.96e-01
39	91	3.0	114	1	GC22_HUMAN	GRANULOCYTE CHEMOTACTI	1.60e+00
40	92	3.0	252	1	POOC_AICCA	COENZYME PQQ SYNTHESIS	1.16e+00
41	92	3.0	464	1	SRPX_HUMAN	SUSRI REPEAT-CONTAININ	1.16e+00
42	91	3.0	505	1	KIR2_HUMAN	SERINE/THROMBIN-PROTE	1.60e+00
43	90	3.0	527	1	SPUB_SERMA	IRON(II)-TRANSPORT SY	2.22e+00
44	91	3.0	651	1	PTSA_MYCPN	PHOSPHATE TRANSPORT SY	1.60e+00
45	91	3.0	960	1	FGD1_MOUSE	PUTATIVE RHO/RAC GUANI	1.60e+00

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	465 AA.
AC	NRTN_CHICK	013157:			
DT	01-NOV-1997	(REL. 35, CREATED)			
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)			
DE	NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GDNF				
DE	RECEPTOR BETA) (GDNFR-BETA).				
GN	GFR2 OR GDNFRB.				
OS	GALLUS GALLUS (CHICKEN).				
OC	EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;				
OC	GALLIFORMES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN;				
RA	BUY-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,				
RA	ROSENTHAL A., CHINCHETRU M., BUCHAN V.L., DAVIES A.M.;				
RL	NATURE 387:721-724(1997).				
CC	-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED				
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO AN...				
CC	TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE				
CC	RECEPTOR (BY SIMILARITY).				
CC	-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.				
CC	-I- SIMILARITY: BELONGS TO THE GDNFR FAMILY.				
DR	EMBL: U90542; G2213805; -				
KW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.				
FT	SIGNAL	1	21	POTENTIAL.	
FT	CHAIN	22	445	NEURTURIN RECEPTOR ALPHA.	
FT	PROPEP	446	465	HYDROPHOBIC. REMOVED DURING MATUR...	
FT				(POTENTIAL).	
FT	CARBOHYD	355	355	POTENTIAL.	
FT	CARBOHYD	387	387	POTENTIAL.	
FT	CARBOHYD	412	412	POTENTIAL.	
FT	LIPID	445	445	GPI-ANCHOR (POTENTIAL).	
SO	SEQUENCE	465 AA;	51908 MW;	5CA073E4 CRC32;	

Query Match 24.7%; Score 750; DB 1; Length 465;
Best Local Similarity 35.5%; Pred. No. 3.47e-155;
Matches 125; Conservative 93; Mismatches 109; Indels 25; Gaps 1

DB	9	TYLVDETLRSLAAPPSPGDLQG-WRPVVCIRANKLAEGSCSSRYRLRQIA...	
OY	13	VYLMILLPLP-SPLPLAGDPLPESRLMNSCLQARRCQADPTCSAAYHLDST...	
DB	67	RDR-NTMLAN--KECOALEVLEOESPLYDCRCGRKREKLOYYWSHGLAAR...	
OY	72	STPLPSEEPSPADCLLEAAQOLRNSSLICGCHRRKKNQVACLDIYVYHRAK...	

```

Db 123 YEASPEYPTSRSLDIFRLASIFSGMDPATNSKNHCLDAKACNLNDCKRLASGYIST 182
QY 132 DVSPYEDVT--SKPMKN-NL-SKLN-MLKPDSDCLCFAMLCITLNDKCDRLKAYGEA 185
Db 183 CSKEISAEHCGRKCHNALROFNDVSEYTYRLFCSC--KDAQCEPRROTIVPICS 240
QY 186 CS---GP--HCORHVCRLQLLTFEFKAEPAHQGLLCPACPNDRGCGERRRNTIAPNCA 240
Db 241 YEDKPNCLDLRNYCRADHLCRSLADPHANCOASFOSTGCPDNDQACLGSTGLIG 300
QY 241 LPVA-PNCLERLRCFSDPLCRSLVDFOTCHP-MDLGTCAEQSR-CIRATLGLIG 297
Db 301 EMDTNYVDASTITITISPCSCSGNLECEKFLRDTENPCLRNAIOA 352
QY 298 TMTNPNFASNTVSALS--CTCRSGNLECEKFLRDTENPCLRNAIOA 347

RESULT 2
ID GDNF_CHICK STANDARD: PRT: 469 AA.
AC 013156:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (TGF-BETA RELATED
DE NEUROTROPHIC FACTOR RECEPTOR 1).
GN GFRA1 OR GDNFR.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RA BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
RA ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
RL NATURE 387:721-724(1997).
CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
CC SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC DR EMBL: U90541; G2213803; -
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
FT SIGNAL 1 27
FT CHAIN 28 430
FT PROPEP 431 469
FT DOMAIN 361 368
FT CARBOHYD 62 62
FT CARBOHYD 163 163
FT CARBOHYD 346 346
FT CARBOHYD 405 405
FT LIPID 430 430
FT SEQUENCE 469 AA; 52043 MW; C8D241C9 CRC32;

Query Match 24.6%; Score 746; DB 1; Length 469;
Best Local Similarity 36.7%; Pred. No. 3,726-154;
Matches 127; Conservative 69; Mismatches 132; Indels 18; Gaps 15;

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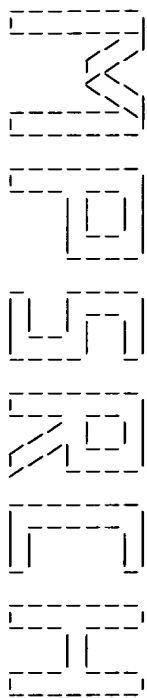
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QY 132 DVSPYE--DVTSKPMKN-LSKLMLKPDSDCLCFAMLCITLNDKCDRLKAYGEA-S 187
Db 180 STSMEICKRCHNALRFLFPKVPKSYGLFESC--RDVACERRROTIVPICSIEDR 237
QY 188 G-PH--CORHVCRLQLLTFEFKAEPAHQGLLCPACPNDRGCGERRRNTIAPNCA 240
Db 238 EKPCLNLOESCKRNYICRSLADFTNCOESRSVSCLEKNYADCLLAVSGLGIVM 240
QY 245 A-PNCLERLRCFSDPLCRSLVDFOTCHPMDI-LGTCAEQ-SRLRAYLGLTGA 347
Db 298 PNVDSSLSVAPWCDCSNGNDIDECRFLNFDOTCKRNAIOA 343
QY 302 PNFASTNVTVSALSCITCRSGNLECEKFLRDTENPCLRNAIOA 347

RESULT 3
ID NRTN_MOUSE STANDARD: PRT: 463 AA.
AC 008842:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
DE (GDNF-BETA).
GN GFRA2 OR GDNFRB OR TRNR2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA BALON R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HEUCKEROH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
RA JOHNSON E.M.JR., MIERANDT J.;
RL NEURON 18:793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
CC AND IN THE ADRENAL.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC DR EMBL: AF002701; G2145082; -
KW MGD; MGI:1195462; GFRA2.
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 21
FT CHAIN 22 443
FT PROPEP 444 463
FT CARBOHYD 52 52
FT CARBOHYD 357 357
FT CARBOHYD 413 413
FT LIPID 443 443
FT VARSUCLC 14 146
FT SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32;

Query Match 23.3%; Score 707; DB 1; Length 463;
Best Local Similarity 36.2%; Pred. No. 3,976-144;
Matches 117; Conservative 83; Mismatches 96; Indels 27; Gaps 15;

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Mparch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 10:00:56 1999; Maspar time 355.59 Seconds
847.489 Million cell updates/sec

Tabular output not generated.

Title: >US-08-866-354-39
Description: (1-2215) from US08866354.seq
Perfect Score: 2215
N.A. Sequence: 1 GCGGCGCGCTGACCTTGAC.....ACAGACTCGACGCGCGCGC 2215
Comp: GCGGCGCGCTGACCTGACCTG.....TGCTGCACTGCGCGCGCGC

Scoring table: TABLE default
Gap 6

Nmatch STD: Dbase 0: Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.676; Variance 5.422; scale 1.785

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1159	52.3	1888	39	Human Ret ligand retL	0.00e+00
2	285	12.9	453	37	Human EST-derived seq	1.23e-185
3	246	11.1	351	37	Human EST-derived seq	1.90e-156
4	213	9.6	2138	38	Rat glial cell line-d	6.89e-132
5	213	9.6	3616	39	Rat Ret ligand retL1	6.89e-132
6	211	9.5	2378	37	Rat glial cell derive	2.10e-130
7	210	9.5	2568	38	Human glial cell line	1.16e-129
8	175	7.9	201	37	Human EST-derived seq	8.03e-104
9	175	7.9	201	37	Human EST-derived seq	8.03e-104
10	166	7.5	1223	39	Human Ret ligand retL	3.22e-97
11	166	7.5	1682	39	Human Ret ligand retL	3.22e-97
12	125	5.6	840	37	Mouse GDNF alpha c10	1.94e-57
13	49	2.2	14704	3	PKS 741 Insert contg.	4.25e-15

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
14	49	2.2	14704	3	PKS 741 Insert contg.	4.25e-15
15	46	2.1	91	29	Repeat sequence from	3.26e-13
16	46	2.1	200	29	Polymorphic repeat se	3.26e-13
17	46	2.1	219	4	Fragile X diagnostic	7.74e-14
18	47	2.1	282	4	Fragile X diagnostic	7.74e-14
19	47	2.1	3381	33	Porphylin-accumulatin	7.74e-14
20	47	2.1	3383	28	Porphylin-accumulatin	7.74e-14
21	46	2.1	10266	22	Mouse SRX-related gen	1.16e-129
22	44	2.0	70	5	Microsatellite sequen	1.16e-129
23	44	2.0	86	5	Microsatellite sequen	1.16e-129
24	44	2.0	91	9	Oligonucleotide prim	1.16e-129
25	45	2.0	266	4	Fragile X diagnostic	1.16e-129
26	45	2.0	382	10	Grasvine ribosomal c	1.16e-129
27	45	2.0	448	35	Penaeus vannamei geno	1.16e-129
28	45	2.0	2775	25	Rat androgen receptor	1.16e-129
29	44	2.0	3404	4	Rat dopamine transpor	1.16e-129
30	44	2.0	3791	29	Chicken beta-actin pr	1.16e-129
31	45	2.0	4157	40	5-aminolevulinic acid	1.16e-129
32	45	2.0	4157	40	Aspergillus oryzae 5-	1.16e-129
33	44	2.0	4253	34	Human MLN 51 nucleoti	1.16e-129
34	45	2.0	13011	35	CDNA encoding rat cyt	1.16e-129
35	43	1.9	61	29	Repeat sequence from	2.34e-11
36	43	1.9	64	5	Microsatellite sequen	2.34e-11
37	43	1.9	65	29	Repeat sequence from	2.34e-11
38	43	1.9	89	29	Repeat sequence from	2.34e-11
39	43	1.9	230	29	Polymorphic repeat se	2.34e-11
40	43	1.9	1570	17	Mouse B7-1 exons 1, 3	2.34e-11
41	43	1.9	1606	17	Mouse B7-1 exons 1, 2	2.34e-11
42	43	1.9	1888	17	Mouse B7-1 exons 1, 2	2.34e-11
43	43	1.9	2446	17	Rat biglycan cDNA.	2.34e-11
44	43	1.9	2516	17	Mouse B7-1 exons 1, 2	2.34e-11
45	43	1.9	2997	17	Murine osteogenic pro	2.34e-11

ALIGNMENTS

RESULT 1
ID V00248 standard; cDNA; 1888 BP.

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
AC	21-MAY-1998	(first entry)				
DE	Human Ret ligand retL2 cDNA.					
KW	Ret ligand; RetL; RetL2; receptor; signal transduction; human;					
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;					
KW	kidney transplant; toxic injury; hypoxic injury;					
KW	neurodegeneration; motor neuron disease; multiple sclerosis;					
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;					
KW	cerebral nerve injury; spinal cord injury; Down's syndrome;					
KW	myasthenia gravis; tumour; therapy; ss.					
OS	Homo sapiens.					
FT	Key	Location/Qualifiers				
FT	CDS	25..1419				
FT		/*tag= a				
PN	MO9744356-A2.					
PD	27-NOV-1997.					
PR	07-MAY-1997; U07726.					
PR	10-APR-1997; US-017427.					
PR	08-MAY-1996; US-017427.					
PR	07-JUN-1996; US-019300.					
PR	16-JUL-1996; US-021859.					
PA	(BIOD) BIOGEN INC.					
PI	Cate RL, Hession C, Santicola-Nadel M;					
DR	WPI; 98-018431/02.					
DR	P-PDB: W37460.					
PT	New nucleic acid encoding ret receptor ligands and related proteins					
PT	- vectors, transformed cells and antibodies, used for promoting cell					
PT	growth and improving survival of injured cells, especially renal or					
PT	nerve cells					
PS	Claim 1: Page 66-69; 113pp; English.					
CC	This sequence comprises cDNA coding for human Ret ligand (RetL)					
CC	RetL2 (see W37460), a key component of the Ret signalling pathway.					
CC	It was isolated from a human foetal liver cDNA library by screening					
CC	with probes (see T99532-33) based on an EST identified using rat					

CC This DNA sequence comprises a human EST-derived sequence designated
 CC y170a10.r1. It can be used to identify glial cell derived
 CC neurotrophic factor receptor (GDNFR) sequences, including human
 CC variants. Also suitable as probes for GDNFR sequences are another
 CC human EST-derived sequence designated y83h05.r1 (see T84978), and
 CC fragments of these EST-derived sequences (see T84980-81) or
 CC proteins encoded by them. The invention relates to novel uses of
 CC GDNFR and its receptor. In particular, it relates to native rat
 CC GDNFR alpha (see W27327), its variants and soluble derivatives
 CC (extracellular domain), chimeric GDNFR alpha and antibodies which
 CC bind to the GDNFR alpha, including agonist and neutralising
 CC antibodies, as well as various uses for these molecules. It also
 CC relates to assay systems for detecting ligands to GDNFR alpha,
 CC systems for studying the physiological role of GDNF, diagnostic
 CC techniques for identifying GDNF-related conditions, methods for
 CC identifying molecules homologous to GDNFR alpha, and claimed
 CC methods for the treatment of GDNF-related and GDNFR alpha-related
 CC conditions, particularly kidney disease associated with
 CC glomerulonephritis and enteric nervous system related disorders.
 CC Transgenic and knockout animals are also claimed.
 CC Sequence 453 BP; 86 A; 152 C; 121 G; 91 T;

Query Match 12.9%; Score 285; DB 37; Length 453;
 Best Local Similarity 87.4%; Pred. No. 1,236-185;
 Matches 396; Conservative 0; Mismatches 46; Indels 11; Gaps 11;

DB 1 gcaaccattgctggaagctgcaaggctgcaacctgaatgaacaactgcaagaagctgc 60
 OY 1144 GCAACCACTGCTGGATGCCCAAGGCTGCAACCTGAATGAACACGCAAGAGCTTC 1203
 DB 61 gctctctacatctccatctgcaacgagagatctgcccacgagagctgcaacgagc 120
 OY 1204 GCTCTCTTAATCTCCATCTGCAACCTGAGATCTCTCCACCGAACGCTGCAACGCC 1263
 DB 121 gcaagtgccacaagagccctgagccagttcttcgacggggtgcccagagatgacac 180
 OY 1264 GCAAGTGCCACAGAGCTGGCGCAGTCTTTGACCGGTGCGCCAGAGATACCTACC 1323
 DB 181 gcatgctctctgctctgcaagaacgagcgctgctgagcgcgcgagcaaacatcc 240
 OY 1324 GCATGCTCTTCTGCTCTGTCAGAGCAGCATGTGTGACGCTGCGCGGCAAAACATCC 1383
 DB 241 tggccagctgctctcctaaggaagaagagcccaactgctcgtgagctgctgagctgt 300
 OY 1384 TGCCAGTGTCTCTATAGAGCAAGAGAACCCCACTGCTGAGACTTGGCAACCTGT 1443
 DB 301 gccgagctgcaacacctgtgtcgtgctcggctngccgacttccatccaattgttcgag 360
 OY 1444 GTCGACAGACCACTGTGCGGGTCCGACTGGAGAG-TTTCACAGCCCACT-GT-CGAG 1500
 DB 361 ccttcctaccagaagaggtcaccagagctcctcctngcgacaattaccagagcggtctg 420
 OY 1501 CCT-CCTACCGGACAA-TCACCAG-CTGTCTT-GCGGACAACT-ACCAAG-CATGTCT-G 1553
 DB 421 gggtctnatgttgcatgattggttgacat 453
 OY 1554 GGCTCTT-ATGCTGGCATGATTGGGTTGATAT 1585

RESULT 3
 ID T84978 standard: DNA; 351 BP.
 AC T84978;
 DT 27-APR-1998 (first entry)
 DE Human EST-derived sequence y83h05.r1.
 KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
 KW GDNF: human; kidney disease; glomerulonephritis; therapy; EST;
 KW expressed sequence tag; ss.
 OS Homo sapiens.
 PN W09733912-A2.
 PD 18-SEP-1997.
 PF 13-MAR-1997; U04363.
 PR 14-MAR-1996; US-618236.
 PR 14-MAR-1996; US-615902.

PA (GETH) GENENTECH INC.
 PI Klein RD, Moore MW, Rosenthal A, Ryan AM;
 DR WPI: 97-470819/43
 PT Isolated glial cell derived neurotrophic factor receptor alpha -
 PT useful to develop products to diagnose and treat associated
 PT disorders, particularly enteric nervous system or kidney disorders
 PS Example 1; Page 61; 100pp; English.
 CC This DNA sequence comprises a human EST-derived sequence designated
 CC y83h05.r1. It can be used to identify glial cell derived
 CC neurotrophic factor receptor (GDNFR) sequences, including human
 CC variants. Also suitable as probes for GDNFR sequences are another
 CC human EST-derived sequence designated y170a10.r1 (see T84979), and
 CC fragments of these EST-derived sequences (see T84980-81) or
 CC proteins encoded by them. The invention relates to novel uses of
 CC GDNFR and its receptor. In particular, it relates to native rat
 CC GDNFR alpha (see W27327), its variants and soluble derivatives
 CC (extracellular domain), chimeric GDNFR alpha and antibodies which
 CC bind to the GDNFR alpha, including agonist and neutralising
 CC antibodies, as well as various uses for these molecules. It also
 CC relates to assay systems for detecting ligands to GDNFR alpha,
 CC systems for studying the physiological role of GDNF, diagnostic
 CC techniques for identifying GDNF-related conditions, methods for
 CC identifying molecules homologous to GDNFR alpha, and claimed
 CC methods for the treatment of GDNF-related and GDNFR alpha-related
 CC conditions, particularly kidney disease associated with
 CC glomerulonephritis and enteric nervous system related disorders.
 CC Transgenic and knockout animals are also claimed.
 CC Sequence 351 BP; 77 A; 117 C; 96 G; 57 T;

Query Match 11.1%; Score 246; DB 37; Length 351;
 Best Local Similarity 89.0%; Pred. No. 1,906-156;
 Matches 276; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

DB 40 ccaagagcaacattgctggaagctgcaaggctgcaacctgaatgaacaactgcaaga 99
 OY 1138 CCAAAAGCAACCACTGCTGGATGCCCAAGGCTGCAACCTGAATGAACACTGCAAGA 1197
 DB 100 agctgagctctctacatctcactgcaacgagagatctgcccacgagcgctgca 159
 OY 1198 AGCTTCTCTCTTATATCTCATCTGCAACCGTGAATCTCTCCACCGAACGCTGCA 1257
 DB 160 accgcgcaagtgccacaagagccctgagccagttcttcgacggggtgccagcagatca 219
 OY 1258 ACCGCCCAAGTGCCACAAGGCTGTGGCCAGTCTTTGACCGTGTGCCACGAGATATA 1417
 DB 220 cctacgcgatgctctctgctcctgccaagatcagcgctgctgagcncgganacaaa 279
 OY 1318 CCTACCGCATGCTCTTCTGCTCTGTCAGAGCAGCATGTGTGACGCTGCCGCGCAA 1477
 DB 280 ccattcctgcccagctgtctcctaaggaagaagagcccaactgntgaacttggag 339
 OY 1378 CCATCTGCCCCAGTGTCTCTATAGAGCAAGAGAACCCCACTGCTGAGACTG 1477
 DB 340 gcgltgtcg 349
 OY 1438 GCCTGTGTCG 1447

RESULT 4
 ID T95297 standard: CDNA; 2138 BP.
 AC T95297;
 DT 01-MAY-1998 (first entry)
 DE Rat glial cell line-derived neurotrophic factor receptor cDNA.
 KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy; ss.
 OS Rattus sp.
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 302..1708
 FT /*tag= a
 FT /product= GDNF_receptor

QY 1250 ACAGTCACACCGCGCAGATGCGACAGAGCTCTGGCCAGTTCTTGAACCTGTGCCAG 1309
DB 1154 caagcacagcgaaggaagcctctctctctcgcgcgaagcctcctcacaagaagcag 1213
QY 1310 CGAGATACCTACCGCATGCTCTCTCTCTGTCAGGACCAAGGAGTCTGTAGCGCG 1369
DB 1214 gcgcacagcctcctctctctctctcctcctcctcctcctcctcctcctcctcctc 1273
QY 1370 CCGGCAACCATCTCGCCCACTGTCTCTATGAGACAGAGAGAGAGCCCACTGCTGCA 1429
DB 1274 ttgcagagcctcctcgaagcgaattacatctcagatcctcgccttcggaattttac 1333
QY 1430 CCGGCGAGCTGTCT 1489
DB 1334 caattgcagcagcgaagcgaagcctcctcctcctcctcctcctcctcctcctcct 1393
QY 1490 CAAGCTGTGAGCT 1549
DB 1394 cctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1453
QY 1550 TCTGGGCT 1609
DB 1454 tagc-ct--gtg-tggcccaatggtgctcgcagcgaagcagtggaagcactaga 1507
QY 1610 CCCCACGGGCGATCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1669
DB 1508 agagtgctgaatttgaatttctcctcctcctcctcctcctcctcctcctcctcct 1567
QY 1670 AGAGTGATGAGATCT 1729
DB 1568 agccttgcaatgctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1599
QY 1730 GGCCTTGTCT 1761

RESULT 8
ID T84980 standard; DNA; 201 BP.
AC T84980:
DE Human EST-derived sequence y8b3h05.r1 fragment.
KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
KW GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
KW expressed sequence tag; ss.
OS Homo sapiens.
PN MO9733912-A2.
PD 18-SEP-1997.
PF 13-MAR-1997; U04363.
PR 14-MAR-1996; US-618236.
PR 14-MAR-1996; US-615902.
PA (GETH) GENENTECH INC.
PI Klein RD, Moore MM, Rosenthal A, Ryan AM;
DR WPI; 97-470819/43.
PT Isolated glial cell derived neurotrophic factor receptor alpha -
PT useful to develop products to diagnose and treat associated
PT disorders, particularly enteric nervous system or kidney disorders
PS Example 1; Page 61; 100pp; English.
CC This DNA sequence comprises a fragment of a human EST-derived
CC sequence designated y8b3h05.r1 (see T84978). It can be used as
CC a probe to identify glial cell derived neurotrophic factor receptor
CC (GDNFR) sequences, including human variants. The invention relates
CC to novel uses of GDNF and its receptor. In particular, it relates
CC to rat GDNFR alpha (see W27327), its variants and soluble derivatives
CC (extracellular domain), chimeric GDNFR alpha and antibodies which
CC bind to the GDNFR alpha, including agonist and neutralizing
CC antibodies, as well as various uses for these molecules. It also
CC relates to assay systems for detecting ligands to GDNFR alpha,
CC systems for studying the physiological role of GDNF, diagnostic
CC techniques for identifying GDNF-related conditions, methods for
CC identifying molecules homologous to GDNFR alpha, and claimed
CC methods for the treatment of GDNF-related and GDNFR alpha-related
CC conditions, particularly kidney disease associated with
CC glomerulonephritis and enteric nervous system related disorders.
CC Transgenic and knockout animals are also claimed.

SQ Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;
Query Match 7.9%; Score 175; DB 37; Length 201;
Best Local Similarity 94.0%; Pred. No. 8.03e-104;
Matches 187; Conservative 0; Mismatches 12; Indels 0; Gap
DB 1 gcaacccatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 60
QY 1144 GCAACCATCT 1203
DB 61 gctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 120
QY 1204 GCTCTCTTATCT 1263
DB 121 gcaagtcgcaagcagcctcctcctcctcctcctcctcctcctcctcctcctcctc 180
QY 1264 GCAAGTCCACAGGCT 1323
DB 181 gcatgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 199
QY 1324 GCATGCT 1342

RESULT 9
ID T84981 standard; DNA; 201 BP.
AC T84981:
DE Human EST-derived sequence y170a10.r1 fragment.
KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
KW GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
KW expressed sequence tag; ss.
OS Homo sapiens.
PN MO9733912-A2.
PD 18-SEP-1997.
PF 13-MAR-1997; U04363.
PR 14-MAR-1996; US-618236.
PR 14-MAR-1996; US-615902.
PA (GETH) GENENTECH INC.
PI Klein RD, Moore MM, Rosenthal A, Ryan AM;
DR WPI; 97-470819/43.
PT Isolated glial cell derived neurotrophic factor receptor alpha -
PT useful to develop products to diagnose and treat associated
PT disorders, particularly enteric nervous system or kidney disorders
PS Example 1; Page 61; 100pp; English.
CC This DNA sequence comprises a fragment of a human EST-derived
CC sequence designated y170a10.r1 (see T84979). It can be used as
CC a probe to identify glial cell derived neurotrophic factor receptor
CC (GDNFR) sequences, including human variants. The invention relates
CC to novel uses of GDNF and its receptor. In particular, it relates
CC to rat GDNFR alpha (see W27327), its variants and soluble derivatives
CC (extracellular domain), chimeric GDNFR alpha and antibodies which
CC bind to the GDNFR alpha, including agonist and neutralizing
CC antibodies, as well as various uses for these molecules. It also
CC relates to assay systems for detecting ligands to GDNFR alpha,
CC systems for studying the physiological role of GDNF, diagnostic
CC techniques for identifying GDNF-related conditions, methods for
CC identifying molecules homologous to GDNFR alpha, and claimed
CC methods for the treatment of GDNF-related and GDNFR alpha-related
CC conditions, particularly kidney disease associated with
CC glomerulonephritis and enteric nervous system related disorders.
CC Transgenic and knockout animals are also claimed.
SQ Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;
Query Match 7.9%; Score 175; DB 37; Length 201;
Best Local Similarity 94.0%; Pred. No. 8.03e-104;
Matches 187; Conservative 0; Mismatches 12; Indels 0; Gap

DB 1 gcaacccatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1
QY 1144 GCAACCATCT 1
DB 61 gctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1
QY 1204 GCTCTCTTATCT 1

Db	121	gcaagtcacaaagccctcgcagttcttcgtgaccgggtgccagcaggtacacctac	180
Yy	1264	GCAAGTGCACAAAGGCTCTCCGCAAGTCTTTGACGTGTGCCGACAGTATACCTAC	1323
Dd	181	gcacgtctctctgctctg	199
Oy	1324	GCATGCTCTTCTGCTCTG	1342
RESULT	10		
ID	V00246	standard: cDNA: 1223 BP.	
AC	V00246		
DT	21-MAY-1998	(first entry)	
DE	Human Ret ligand: retL partial cDNA.		
KW	Ret ligand; RetL; RetL; receptor; signal transduction; human;		
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;		
KW	kidney transplant; toxic injury; hypoxic injury;		
KW	neurodegeneration; motor neurone disease; multiple sclerosis;		
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;		
KW	cerebral nerve injury; spinal cord injury; Down's syndrome;		
KW	cerebral palsy; Lyme disease; muscular dystrophy;		
KW	amshethia gravis; tumour; therapy; ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	1..1041	
FT	CDS	/*tag= a	
PN	W09744356-A2.		
PF	27-NOV-1997.		
PR	07-MAY-1997: U07726.		
PR	10-APR-1997: U5-017427.		
PR	08-MAY-1996: U5-017427.		
PR	07-JUN-1996: U5-019300.		
PR	16-JUL-1996: U5-021859.		
PA	(BIOJ) BIOGEN INC.		
PI	Cate RL, Hession C, Sanicola-Nedel M;		
DR	WPI: 98-018431/02.		
DR	P-PSDB: W37458.		
PT	New nucleic acid encoding ret receptor ligands and related proteins		
PT	- vectors, transformed cells and antibodies, used for promoting cell		
PT	growth and improving survival of injured cells, especially renal or		
PT	nerve cells		
PS	Claim 1: Page 58-60: 113pp; English.		
CC	This sequence comprises a partial cDNA for human Ret ligand (RetL)		
CC	RetL (see W37458), a key component of the Ret signalling pathway.		
CC	It was isolated from a human embryonic kidney cDNA library using		
CC	ret retL cDNA (see V00245) as probe. A full-length sequence (see		
CC	V00247) for human retL cDNA has also been obtained, as well as		
CC	mouse and human retL2 and retL3 sequences (see V00248-51). Vectors		
CC	containing retL DNA and prokaryotic or eukaryotic host cells		
CC	transformed or transfected with these vectors are claimed, as well		
CC	as a method for production of RetL, its soluble variants and		
CC	fusion proteins with a toxin, imageable compound or radionuclide.		
CC	RetL, optionally when expressed from vectors in vivo, is used to		
CC	promote growth of new tissue and survival of damaged tissue,		
CC	particularly kidney or neural tissue. Typical applications are in		
CC	renal failure, nephritis, kidney transplants, toxic or hypoxic		
CC	injury, neurodegeneration, motor neurone disease, multiple		
CC	sclerosis, bacterial, viral or prion infections (e.g. meningitis,		
CC	myelopathy associated with HIV or Creutzfeldt-Jakob disease),		
CC	cranial nerve or spinal cord injury, developmental disorders such		
CC	as Down's syndrome and cerebral palsy, or conditions involving the		
CC	peripheral nervous system (Lyme disease, muscular dystrophy and		
CC	Amshethia gravis). Fusion proteins are used to deliver toxins		
CC	etc. to Ret-expressing cells, especially tumours.		
CC	Sequence 1223 BP: 323 A; 329 C; 274 G; 297 T;		
SO			
Query Match	7.5%; Score 166; DB 39; Length 1223;		
Best Local Similarity	66.8%; Pred. No. 3, 22e-97;		
Matches	420; Conservative 0; Mismatches 200; Indels 9; Gaps		
Db	84	catcccaagaaggaaacactgctgatacgcagcgaagcctgcaacctgacacattg	143

QY	1133	CAGTACCAAAGACACACACTGCTTGGATATGCGGCAAGGCGCTTCAACCTGATGACAACTG	1142
Db	144	caagaagatcacagtcgagcgatcacatcccccgtgca-ccaccagc-igtccaac-gatyl	200
QY	1193	CAGAAGAGTGGCTCTCTATTATATCTCATATCTCAACCGGTGAGATCTCTCCACACGAAAG	1242
Db	201	ctgcacaacgcgcgaagatgcccacaagaagcccttcggcagatctctttgtccaaaggtcccgacaa	257
QY	1233	CTGCACACGCCGCAAGTGGCCACCAAGGCTCTGGCCCAAGTCTTTTGACCGTGTGCTCAATG	1292
Db	261	gcacagctcaggaatgtctctcttcgcccttcgcccggagacatgcgctccacaagaagcagagaa	317
QY	1313	GATATACCTACACGATGCTCTTCTGCTCTGTACAGAACACGGCATGTGCTGACGTCGCGC	1362
Db	321	acagaccatcgtgcctcgtgtgctctcctatgaagaagaggagaaagcccaactgtttgaatt	380
QY	1373	GCAAAACATCTCTGCCAGTGTGCTCTATGAGGACAAAGGAAGGCCCACTGGCTGGACCT	1432
Db	381	gcaggaactctctcagaagaacgaattacatctgcagatctgcctctcggaattttttaccaa	440
QY	1433	GCGCAGCGCTGTGTGTGTACACACCCTGTGCGCGGTCCGACATGCGAGATTTCACGCCAA	1492
Db	441	ctgcgcagccacagatgcacaagatgcctcagcagctgtctcaagaagaaactacgcctgaact	500
QY	1493	CTGTGAGCCTCTTACCGGCAATACACAGCTGTCTCGGCAACTATCCAGGCACTGTGCT	1552
Db	501	ccctgcctactcgggggtctttcttgacaagtcatacgaaccccaactacatagactcagtag	560
QY	1553	GGGCGCTCATATGCTGGCATGTATGGTTGATATGACACCCACATATGTGAGCTCCAAACC	1612
Db	561	c-ct--gtg-tggcccactgtgtgtgactgcagcaacagctggagacgacctagaaga	614
QY	1613	CACGGCGATCTGTGTGTCTCTCCCTGTGCAATTGTCTGTGGCACTGGGAACATGGAAGA	1672
Db	615	gtgtcttgaaatttttgattcttctcaaggacaatcagctcttaaaatgcaattcaagc	674
QY	1673	GTTGAGAGAAAGTCTCTCAGGACCTTCACGGAAACCCCATGCTCCGGAATGCCATTCAAGC	1732
Db	675	ctttgcgaatggtcctccgatgtgacgctgt	703
QY	1733	CTTTGATATGCGACACAGATGTGAACATGT	1761
RESULT	11		
ID	V00247	standard; cDNA; 1682 BP.	
AC	V00247;		
DT	21-MAY-1998	(first entry)	
DE	Human Ret ligand retL cDNA.		
KW	Human Ret ligand retL; cDNA.		
KW	Ret ligand; RetL; receptor; signal transduction; human;		
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;		
KW	kidney transplant; toxic injury; hypoxic injury;		
KW	neurodegeneration; motor neurone disease; multiple sclerosis;		
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;		
KW	cerebral nerve injury; spinal cord injury; Down's syndrome;		
KW	cerebral palsy; Lyme disease; muscular dystrophy;		
KW	myasthenia gravis; tumour; therapy; ss.		
OS	Homo sapiens.		
FT	Key	location/Qualifiers	
FT	CDS	118..1500	
FT		/*tag= a	
PN	MO3744356-A2.		
PD	27-NOV-1997.		
PR	07-MAY-1997; U07726.		
PR	10-APR-1997; US-017427.		
PR	08-MAY-1996; US-017427.		
PR	07-JUN-1996; US-019300.		
PR	16-JUL-1996; US-021859.		
PA	(BioC) BIOGEN INC.		
PI	Catec RL, Hession C, Santicola-Nedel M;		
DR	WPI: 98-018431/02.		
DR	P-PSDS: W37459.		
PT	New nucleic acid encoding ret receptor ligands and related proteins		

PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 1: Page 62-64: 113bp: English.
CC This sequence comprises cDNA coding for human Ret 1192 (Ret1).
CC Ret1 (see W37459), a key component of the Ret signaling pathway.
CC It was deduced from 2 clones isolated from human foetal kidney.
CC cDNA using primers based on a partial human Ret1 cDNA (see
CC V00246). Rat Ret1 and mouse and human Ret1 and Ret2 sequences
CC have also been identified (see V00245 and V00248-51). The human
CC Ret1 cDNA is 88.28 identical to rat Ret1 cDNA. Vectors
CC containing Ret1 DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of Ret1. Its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC Ret1, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving the
CC peripheral nervous system (Lyme disease, muscular dystrophy and
CC peripheral neuropathy). Fusion proteins are used to deliver toxins
CC etc. to Ret-expressing cells, especially tumours.
SO Sequence 1682 BP: 417 A: 461 C: 433 G: 371 T:

Query Match 7.5%; Score 166; DB 39; Length 1682;
Best Local Similarity 66.8%; Pred. No. 3.22e-97;
Matches 420; Conservative 0; Mismatches 200; Indels 9; Gaps 7;

Db 543 catcccaaaagggaacacacgctgctgagcgaagagcctgcacactgcagcattg 602
Qy 1133 CAGTACCAAAAGCAACACCTCCGATGCGCGCAAGGCTCGCACTGATGACCACTG 1192
Db 603 caaagaatcacagcgcgtacacacccgtgca-cacacacagc-ggtccacac-gatgt 659
Qy 1193 CAAAGACTTCGCTCCTTATATCTCATCTGCAACCGTGAATCTCTCCACCGAACG 1252
Db 660 ctgcaacgcgcgcgaagtgcaagagccctcgcgcagcttcttgcaaggtccgcgca 719
Qy 1253 CTGCAACGCGCGCAAGTGCCACAGGCTCGCAAGTCTTATGACGCTGCGCCACGA 1312
Db 720 gcaacagctacgaatgtctctctcctcgcgcggaacatgcgcgcagcagcgaggg 779
Qy 1313 GTATACCTACCGCATGCTCTCTCTCTCTGACAGGACCATGCTGAGCGCTGCCG 1372
Db 780 acagacacatgctgctgtgtctctctatgaagagagagagacacatgttgaatt 839
Qy 1373 GCAAAACCATCTGCGCCAGTTCCTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
Db 840 gcaagagctctctgcaagaacgaatcacatctgcagatctgccttgccgattttt 899
Qy 1433 GCGGAGCTGT 1492
Db 900 ctgcaacgcgcgcgaagtgcaagagccctcgcgcagcttcttgcaaggtccgcgca 959
Qy 1493 CTGTCGAGCTCTCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1552
Db 960 cctgcgactcgcgcgcgtatgtgacacatcacacacacacacacacacacacacac 1019
Qy 1553 GGGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1612
Db 1020 c-ct--gtg-tggcccccaatgggtgacacgaacacacacacacacacacacac 1073
Qy 1613 CACGGGATGCTGT 1672
Db 1074 gtgtgtgaaatttttgaaatttttcaagaagaacacacacacacacacacacacac 1133
Qy 1673 GTGTGAGAGTTCTCTGAGGAGCTTACGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1732

Db 1134 ctgtgcaatgctccgacatgacgctgt 1162
Qy 1733 CTTTGGAATGCGACAGATGTGAACATGT 1761

RESULT 12
ID T84977 standard; cDNA: 840 BP.
AC T84977;
DT 27-APR-1998 (first entry)
DE Mouse GDNF alpha clone 26 3' end.
KW Glial cell derived neurotrophic factor receptor alpha; GDNF alpha;
KM GDNF; mouse; kidney disease; glomerulonephritis; therapy; ss.
OS Mus musculus.
PN W09733912-A2.
PD 18-SEP-1997.
PF 13-MAR-1997: U04363.
PR 14-MAR-1996: US-618236.
PR 14-MAR-1996: US-615902.
PA (GETH) GENENTECH INC.
PI Klein RD, Moore MW, Rosenthal A, Ryan AM;
DR WPI: 97-470819/43.
PT Isolated glial cell derived neurotrophic factor receptor alpha;
PT useful to develop products to diagnose and treat associated
PT disorders, particularly enteric nervous system or kidney disorders.
PS Example 1: Page 60-61; 100bp: English.
CC This cDNA sequence comprises the 3' end of mouse full-length
CC glial cell derived neurotrophic factor receptor alpha (GDNF alpha;
CC (see W27327) clone 26; the 5' end of the clone is given in
CC T84978. Clone 26 was isolated from a mouse cDNA library using
CC rat GDNF alpha cDNA (see T84975) as probe. The invention relates
CC to novel uses of GDNF and its receptor. In particular, it relates
CC to native rat GDNF alpha (see W27327), its variants and soluble
CC derivatives (extracellular domain), chimeric GDNF alpha and
CC antibodies which bind to the GDNF alpha, including agonist and
CC neutralising antibodies, as well as various uses for these
CC molecules. It also relates to assay systems for detecting ligands
CC to GDNF alpha, systems for studying the physiological role of
CC GDNF, diagnostic techniques for identifying GDNF-related conditions,
CC methods for identifying molecules homologous to GDNF alpha, and
CC therapeutic techniques (claimed) for the treatment of GDNF-related
CC and GDNF alpha-related conditions, particularly kidney disease,
CC associated with glomerulonephritis and enteric nervous system
CC related disorders. Transgenic and knockout animals are also
CC claimed.
SO Sequence 840 BP: 205 A: 245 C: 200 G: 190 T:

Query Match 5.6%; Score 125; DB 37; Length 840;
Best Local Similarity 64.8%; Pred. No. 1.94e-67;
Matches 339; Conservative 0; Mismatches 178; Indels 6; Gaps 4;

Db 1 cgcgcgaagagcgaacacacgctcgaagcagcttcttgacaaggttcacacacacacac 60
Qy 1260 CGCCGCAAGGCGCAAGAGCTGTGCGCAAGTCTTTGACGCTGCGCAAGGATATAC 1319
Db 61 tacgagatgctcttctgctcctcgcgcgagcgtcgcgcacacacacacacacacac 120
Qy 1320 TACCGCATGCTCTTCTGCTCTCTCTGACAGACAGCATGTCTGAGCTGCGGCAAC 1379
Db 121 atcgtccctgtgtctcctatgaagaacagagagggcccaactgcctgaatctgcaagac 180
Qy 1380 ATCCTCCCGAGTGTCTCTATGAGACAAGAGAACCCCAACTGCTGACCTGCGCAC 1439
Db 181 tcttgcaagacaataatcatctgcagatctgcctgcagatctttttccaactgcag 240
Qy 1440 CTGTGTGCTGACACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1499
Db 241 ccagagatcaaggtctgcac 300
Qy 1500 GCCTCTACCGGACATACACACACCTCTCTGCGGACAACTACACAGCATGTCTGGCT 1559
Db 301 tactcggaactgtgtgcac 357
Qy 1560 TATGCTGCAATGATGTGGGTTTGTATGACACCAACTATGTGACTCAACCCACGAG 1619

Mon Mar 15 06:28:33 1999

US-08-866-354-39.rng

Page 11

Search completed: Fri Mar 12 10:08:30 1999
Job time : 454 secs.

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CC RetL2, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.
CC Sequence 464 AA:

Query Match 93.7%: Score 3131; DB 28; Length 464;
Best Local Similarity 94.3%: Pred. No. 0.00e+00;
Matches 427; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

DB 12 fiderlrlslapspslqgplhgwtrpvdcrnelcaasncsryrlrlgclagrdnt 71
8 YDETLRLSLAPSSLSGSELHGMRPQVDCVRANELCAASNCSSRYRLRLGCLAGRDNT 67
DB 72 mlanecqalevgesplydcrckrmkkelqclqlywsllqltegeefyeaspyepv 131
68 MLANECQALVLESPDYDCRCKRMKKELOCLOIYWSIHGLTEGEFEYASPYEPV 127
DB 132 terlrlslapspslqgplhgwtrpvdcrnelcaasncsryrlrlgclagrdnt 191
128 TRLRLSLAPSSLSGSELHGMRPQVDCVRANELCAASNCSSRYRLRLGCLAGRDNT 187
DB 132 tercnrckhkalrgfdtvpaseylyrmfscsqdgaacaeerrrrqllpscsyedekepn 251
188 TERCNRCKHKAALRGFDTPVASEYLYRMFSCSQDGAACAEERRRRQILLPSCSYEDKEPN 247
DB 252 ldlrgvctthlcrerlrladfnhancasqvtscpadnygacisyaqumlgdmtpryvd 311
248 LDLRGLCRTHLCRSLADFNHANCASQVTSCTPADNYGACISYAQUMLGDMTPRYVD 307
DB 312 ssptlsvspwpcscrgsgnmeceekflrdftfepclnnaqafngndvnsppspfq 371
308 SNPTLSPVSPWPCSCRGSGNMECEKFLRDFTFEPCLNNAQAFNGNDVNSPPSPFP 367
DB 372 atqaprvetpsladdlslstslgsvlttctsvyegglkannskelsmcteltunlp 431
368 ATQAPRVETPSLADDSLSTSLGSVLTCTCTSVYEGGLKANNSKELSMCTELTUNLP 427
DB 432 gsnkvtkpnsgrtrrpsaalvtvslmlkial 464
428 GSKVKTKPNSGRTRRPSAALVTVSLMLKIAL 460

RESULT 2
ID W35334 standard; Protein: 468 AA.
AC W35334;
DT 01-MAY-1998 (first entry)
DE Rat glial cell line-derived neurotrophic factor receptor.
KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
KW gene therapy.
OS Rattus sp.
PN M09740153-A1.
PD 30-OCT-1997.
PF 15-APR-1997; U06281.
PR 14-APR-1997; US-837199.
PR 22-APR-1996; US-015907.
PR 09-MAY-1996; US-017221.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jinn S, Wen D;
DR WPI: 97-535836/49.
DR N-PSDB: T95297.
PT Glial cell line derived neurotrophic factor receptor - useful to

PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and
PT Alzheimer's disease
PS Claim 1; Pages 96-98; 196pp; English.
CC The present sequence is the rat glial cell line-derived
CC neurotrophic factor (GDNF) receptor, which can be used to treat
CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
CC disease or amyotrophic lateral sclerosis, complications of diabetes
CC and Huntington's disease and (optionally in combination with GDNF)
CC glaucoma, retinal degeneration and hearing loss caused by injury to
CC inner ear sensory neurons. The receptor can also be used to block
CC unwanted GDNF activity, analyse GDNF related molecules and
CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
CC cells, preferably transfected ex vivo, can be used similarly by
CC implantation, and the use of the receptor cDNA in gene therapy is
CC also contemplated. Probes based on the cDNA can be used to identify
CC GDNF responsive cells and tissues, e.g. to identify patients who
CC would benefit from GDNF therapy, and abnormalities in receptor
CC expression, and to isolate molecules that form a complex with the
CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
CC antibodies, oligonucleotides derived from the cDNA and animal
CC models that overexpress the receptor can be used to study the
CC biological function of GDNF, knockout transgenic animals can be
CC used to detect GDNF dependent neurons or processes and the antibody
CC can be used in immunoassays for the receptor. The receptor binds
CC GDNF specifically and with high affinity, acting as part of a
CC complex that mediates/enhances signal transduction by GDNF, i.e.
CC increasing dopamine uptake in dopaminergic cells.
CC Sequence 468 AA;

Query Match 46.7%: Score 1560; DB 28; Length 468;
Best Local Similarity 48.8%: Pred. No. 1.20e-147;
Matches 218; Conservative 98; Mismatches 117; Indels 14; Gaps 12;

DB 16 lmsaevsgqdlrdcvkasdqclkegscstkyrlrlgcvagketnfaletsgleakdecrs 74
22 LGSELHGMRPQVDCVRANELCAASNCSSRYRLRLGCLAGRDNT--LM--LANK-ECQA 76
DB 75 ameklkqsklyncrcckgmkkcknccllywamyaslqgnlldspypnrsldlfr 133
77 ALEVLQSPPLDCKCKRMKKELOCLOIYWSIHGLTEGEFEYASPYEPVTSRLSDIFR 136
DB 134 avpfisdvfgqvehlsgkgncldaekcnlddckkyrsayltpcttsms-necnrck 192
137 LASLFGSGTDPANVSTSNHCLDAKACNLNDCKRLRSSITISCNREISPTENCRNKC 190
DB 193 hkalrgfdkvpakhsygmfcscrdiaacterrqtlvpcsyeeerprncslsdgck 247
197 HKALRGFDKVPKHSYGMFCSCRDIAACTERRQTLVPCSYEEERPRNCSLSDGCK 244
DB 253 nylcrsladfnhancasqvtscpadnygacisyaqumlgdmtpryvd--s-lsvn 371
257 DNLCSRLADFNHANCASQVTSCTPADNYGACISYAQUMLGDMTPRYVDSNPTGLVNS 374
DB 311 pwcdrsgnldedclfnffkdnclknlaqafngndvnsppspfq--pqpqtatcttla 431
317 PWCDRSGNMECEKFLRDFTFEPCLNNAQAFNGNDVNSPPSPFP--PAQVQTRV--E 434
DB 371 frvknkplpagsenelphvlpccanlqgklknsygschiclsadfdgkglagase 430
376 -KTPSLPDDSLDSTSLGTSVITTCSTISQEGGLKANNKSKELSMCTELTUNIPGSKV 433
DB 431 hitkmaappscslslpvlmltala 457
434 KINSGSSRRARLSAALTALPLMLT-LA 459

RESULT 3
ID W37457 standard; Protein: 468 AA.
AC W37457;
DT 21-MAY-1998 (first entry)
DE Rat Ret ligand; RetL1; RetL2; RetL3; RetL4; RetL5; RetL6; RetL7;
KW Ret ligand; RetL1; RetL2; RetL3; RetL4; RetL5; RetL6; RetL7;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;

 M P E R E H
 (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Mar 8 14:28:13 1999; Maspar time 23.75 Seconds
 725,580 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-866-354-40
 Description: (1-460) from US08866354.pep
 Perfect Score: 3343
 Sequence: 1 MLVPSHYPDETLRLSLASPS.....RARLSAATLALPLMLTLAL 460

Scoring table:
 PAM 150
 Gap 11

Searched: 116738 segs, 37463448 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r58
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 46.747; Variance 80.467; scale 0.581

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	777	23.2	397	2 JE0082	GPI-linked receptor -	4.61e-149
2	102	3.1	302	1 WZB29	gene 9 protein - huma	1.31e-01
3	103	3.1	1712	1 A38261	masking protein precu	9.37e-02
4	96	2.9	201	2 A47096	response regulator po	9.15e-01
5	97	2.9	344	2 S72723	dipeptide transporter h	6.66e-01
6	98	2.9	430	2 B70518	probable ctna - Mycob	4.83e-01
7	96	2.9	480	2 S52306	zinc finger protein 1	9.15e-01
8	93	2.8	194	2 G64322	hypothetical protein	2.34e+00
9	93	2.8	326	2 G02632	hypoxia-inducible gen	2.34e+00
10	92	2.8	429	2 S13588	malate dehydrogenase	3.18e+00
11	95	2.8	432	1 DEMZWC	malate dehydrogenase	1.25e+00
12	92	2.8	452	2 S62767	translation elongatio	3.18e+00
13	92	2.8	452	2 S68466	translation elongatio	3.18e+00
14	92	2.8	799	1 TVRT1B	neive growth factor r	3.18e+00
15	93	2.8	2871	2 A55674	fibritillin-1 precursor	2.34e+00
16	93	2.8	2871	2 A55674	fibritillin-1 precursor	2.34e+00
17	89	2.7	113	2 C70927	probable rplp protein	7.85e+00
18	90	2.7	272	2 S13587	malate dehydrogenase	5.83e+00
19	89	2.7	282	2 G13334	probable lysophosphat	7.85e+00
20	89	2.7	325	2 A40963	phospholipase A2-acti	7.85e+00
21	91	2.7	342	2 A44965	cysteine proteinase (4.31e+00
22	91	2.7	342	2 A44965	cysteine proteinase (4.31e+00
23	90	2.7	379	2 I57459	galactose-1-phosphate	5.83e+00

24	90	2.7	379	2 A44473	UTP--hexose-1-phospha	5.83e+00
25 <td>91 <td>2.7 <td>381 <td>1 B26359 <td>decay-accelerating fa</td> <td>4.31e+00</td> </td></td></td></td>	91 <td>2.7 <td>381 <td>1 B26359 <td>decay-accelerating fa</td> <td>4.31e+00</td> </td></td></td>	2.7 <td>381 <td>1 B26359 <td>decay-accelerating fa</td> <td>4.31e+00</td> </td></td>	381 <td>1 B26359 <td>decay-accelerating fa</td> <td>4.31e+00</td> </td>	1 B26359 <td>decay-accelerating fa</td> <td>4.31e+00</td>	decay-accelerating fa	4.31e+00
26 <td>91 <td>2.7 <td>428 <td>2 S67176 <td>tRNA isopentenyltrans</td> <td>4.31e+00</td> </td></td></td></td>	91 <td>2.7 <td>428 <td>2 S67176 <td>tRNA isopentenyltrans</td> <td>4.31e+00</td> </td></td></td>	2.7 <td>428 <td>2 S67176 <td>tRNA isopentenyltrans</td> <td>4.31e+00</td> </td></td>	428 <td>2 S67176 <td>tRNA isopentenyltrans</td> <td>4.31e+00</td> </td>	2 S67176 <td>tRNA isopentenyltrans</td> <td>4.31e+00</td>	tRNA isopentenyltrans	4.31e+00
27 <td>90 <td>2.7 <td>430 <td>2 S17781 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td></td></td></td>	90 <td>2.7 <td>430 <td>2 S17781 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td></td></td>	2.7 <td>430 <td>2 S17781 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td></td>	430 <td>2 S17781 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td>	2 S17781 <td>malate dehydrogenase</td> <td>5.83e+00</td>	malate dehydrogenase	5.83e+00
28 <td>90 <td>2.7 <td>432 <td>2 S20743 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td></td></td></td>	90 <td>2.7 <td>432 <td>2 S20743 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td></td></td>	2.7 <td>432 <td>2 S20743 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td></td>	432 <td>2 S20743 <td>malate dehydrogenase</td> <td>5.83e+00</td> </td>	2 S20743 <td>malate dehydrogenase</td> <td>5.83e+00</td>	malate dehydrogenase	5.83e+00
29 <td>90 <td>2.7 <td>463 <td>2 A26652 <td>type 1 site-specific</td> <td>5.83e+00</td> </td></td></td></td>	90 <td>2.7 <td>463 <td>2 A26652 <td>type 1 site-specific</td> <td>5.83e+00</td> </td></td></td>	2.7 <td>463 <td>2 A26652 <td>type 1 site-specific</td> <td>5.83e+00</td> </td></td>	463 <td>2 A26652 <td>type 1 site-specific</td> <td>5.83e+00</td> </td>	2 A26652 <td>type 1 site-specific</td> <td>5.83e+00</td>	type 1 site-specific	5.83e+00
30 <td>89 <td>2.7 <td>493 <td>2 JC5621 <td>epidermal growth fact</td> <td>7.85e+00</td> </td></td></td></td>	89 <td>2.7 <td>493 <td>2 JC5621 <td>epidermal growth fact</td> <td>7.85e+00</td> </td></td></td>	2.7 <td>493 <td>2 JC5621 <td>epidermal growth fact</td> <td>7.85e+00</td> </td></td>	493 <td>2 JC5621 <td>epidermal growth fact</td> <td>7.85e+00</td> </td>	2 JC5621 <td>epidermal growth fact</td> <td>7.85e+00</td>	epidermal growth fact	7.85e+00
31 <td>90 <td>2.7 <td>568 <td>2 S74481 <td>epidermal growth fact</td> <td>5.83e+00</td> </td></td></td></td>	90 <td>2.7 <td>568 <td>2 S74481 <td>epidermal growth fact</td> <td>5.83e+00</td> </td></td></td>	2.7 <td>568 <td>2 S74481 <td>epidermal growth fact</td> <td>5.83e+00</td> </td></td>	568 <td>2 S74481 <td>epidermal growth fact</td> <td>5.83e+00</td> </td>	2 S74481 <td>epidermal growth fact</td> <td>5.83e+00</td>	epidermal growth fact	5.83e+00
32 <td>91 <td>2.7 <td>585 <td>2 S43572 <td>C05B5.5 protein (clon</td> <td>4.31e+00</td> </td></td></td></td>	91 <td>2.7 <td>585 <td>2 S43572 <td>C05B5.5 protein (clon</td> <td>4.31e+00</td> </td></td></td>	2.7 <td>585 <td>2 S43572 <td>C05B5.5 protein (clon</td> <td>4.31e+00</td> </td></td>	585 <td>2 S43572 <td>C05B5.5 protein (clon</td> <td>4.31e+00</td> </td>	2 S43572 <td>C05B5.5 protein (clon</td> <td>4.31e+00</td>	C05B5.5 protein (clon	4.31e+00
33 <td>89 <td>2.7 <td>808 <td>1 VGBESM <td>glycoprotein B precu</td> <td>7.85e+00</td> </td></td></td></td>	89 <td>2.7 <td>808 <td>1 VGBESM <td>glycoprotein B precu</td> <td>7.85e+00</td> </td></td></td>	2.7 <td>808 <td>1 VGBESM <td>glycoprotein B precu</td> <td>7.85e+00</td> </td></td>	808 <td>1 VGBESM <td>glycoprotein B precu</td> <td>7.85e+00</td> </td>	1 VGBESM <td>glycoprotein B precu</td> <td>7.85e+00</td>	glycoprotein B precu	7.85e+00
34 <td>89 <td>2.7 <td>823 <td>2 A36378 <td>probable transcriptio</td> <td>7.85e+00</td> </td></td></td></td>	89 <td>2.7 <td>823 <td>2 A36378 <td>probable transcriptio</td> <td>7.85e+00</td> </td></td></td>	2.7 <td>823 <td>2 A36378 <td>probable transcriptio</td> <td>7.85e+00</td> </td></td>	823 <td>2 A36378 <td>probable transcriptio</td> <td>7.85e+00</td> </td>	2 A36378 <td>probable transcriptio</td> <td>7.85e+00</td>	probable transcriptio	7.85e+00
35 <td>90 <td>2.7 <td>886 <td>2 A57172 <td>probable hormone rece</td> <td>5.83e+00</td> </td></td></td></td>	90 <td>2.7 <td>886 <td>2 A57172 <td>probable hormone rece</td> <td>5.83e+00</td> </td></td></td>	2.7 <td>886 <td>2 A57172 <td>probable hormone rece</td> <td>5.83e+00</td> </td></td>	886 <td>2 A57172 <td>probable hormone rece</td> <td>5.83e+00</td> </td>	2 A57172 <td>probable hormone rece</td> <td>5.83e+00</td>	probable hormone rece	5.83e+00
36 <td>90 <td>2.7 <td>1630</td> <td>2 A53577 <td>ascites staloglycopo</td> <td>5.83e+00</td> </td></td></td>	90 <td>2.7 <td>1630</td> <td>2 A53577 <td>ascites staloglycopo</td> <td>5.83e+00</td> </td></td>	2.7 <td>1630</td> <td>2 A53577 <td>ascites staloglycopo</td> <td>5.83e+00</td> </td>	1630	2 A53577 <td>ascites staloglycopo</td> <td>5.83e+00</td>	ascites staloglycopo	5.83e+00
37 <td>90 <td>2.7 <td>2907</td> <td>2 A57278 <td>fibritillin-2 precursor</td> <td>5.83e+00</td> </td></td></td>	90 <td>2.7 <td>2907</td> <td>2 A57278 <td>fibritillin-2 precursor</td> <td>5.83e+00</td> </td></td>	2.7 <td>2907</td> <td>2 A57278 <td>fibritillin-2 precursor</td> <td>5.83e+00</td> </td>	2907	2 A57278 <td>fibritillin-2 precursor</td> <td>5.83e+00</td>	fibritillin-2 precursor	5.83e+00
38 <td>89 <td>2.7 <td>2918</td> <td>2 A54105 <td>fibritillin-2 precursor</td> <td>7.85e+00</td> </td></td></td>	89 <td>2.7 <td>2918</td> <td>2 A54105 <td>fibritillin-2 precursor</td> <td>7.85e+00</td> </td></td>	2.7 <td>2918</td> <td>2 A54105 <td>fibritillin-2 precursor</td> <td>7.85e+00</td> </td>	2918	2 A54105 <td>fibritillin-2 precursor</td> <td>7.85e+00</td>	fibritillin-2 precursor	7.85e+00
39 <td>90 <td>2.7 <td>3002</td> <td>2 A47221 <td>fibritillin-1 precursor</td> <td>5.83e+00</td> </td></td></td>	90 <td>2.7 <td>3002</td> <td>2 A47221 <td>fibritillin-1 precursor</td> <td>5.83e+00</td> </td></td>	2.7 <td>3002</td> <td>2 A47221 <td>fibritillin-1 precursor</td> <td>5.83e+00</td> </td>	3002	2 A47221 <td>fibritillin-1 precursor</td> <td>5.83e+00</td>	fibritillin-1 precursor	5.83e+00
40 <td>90 <td>2.7 <td>3020</td> <td>2 A43932 <td>mucin 2 precursor, in</td> <td>5.83e+00</td> </td></td></td>	90 <td>2.7 <td>3020</td> <td>2 A43932 <td>mucin 2 precursor, in</td> <td>5.83e+00</td> </td></td>	2.7 <td>3020</td> <td>2 A43932 <td>mucin 2 precursor, in</td> <td>5.83e+00</td> </td>	3020	2 A43932 <td>mucin 2 precursor, in</td> <td>5.83e+00</td>	mucin 2 precursor, in	5.83e+00
41 <td>88 <td>2.6</td> <td>498</td> <td>2 S77665</td> <td>integral membrane pro</td> <td>1.06e+01</td> </td>	88 <td>2.6</td> <td>498</td> <td>2 S77665</td> <td>integral membrane pro</td> <td>1.06e+01</td>	2.6	498	2 S77665	integral membrane pro	1.06e+01
42 <td>88 <td>2.6</td> <td>503</td> <td>4 S23741 <td>hypothetical TPR/TRK</td> <td>1.06e+01</td> </td></td>	88 <td>2.6</td> <td>503</td> <td>4 S23741 <td>hypothetical TPR/TRK</td> <td>1.06e+01</td> </td>	2.6	503	4 S23741 <td>hypothetical TPR/TRK</td> <td>1.06e+01</td>	hypothetical TPR/TRK	1.06e+01
43 <td>88 <td>2.6</td> <td>505</td> <td>2 A57156</td> <td>Ca2+/calmodulin-depen</td> <td>1.06e+01</td> </td>	88 <td>2.6</td> <td>505</td> <td>2 A57156</td> <td>Ca2+/calmodulin-depen</td> <td>1.06e+01</td>	2.6	505	2 A57156	Ca2+/calmodulin-depen	1.06e+01
44 <td>88 <td>2.6</td> <td>790</td> <td>1 TVHUTT</td> <td>neive growth factor r</td> <td>1.06e+01</td> </td>	88 <td>2.6</td> <td>790</td> <td>1 TVHUTT</td> <td>neive growth factor r</td> <td>1.06e+01</td>	2.6	790	1 TVHUTT	neive growth factor r	1.06e+01
45 <td>88 <td>2.6</td> <td>1002</td> <td>2 G70876</td> <td>probable transmembran</td> <td>1.06e+01</td> </td>	88 <td>2.6</td> <td>1002</td> <td>2 G70876</td> <td>probable transmembran</td> <td>1.06e+01</td>	2.6	1002	2 G70876	probable transmembran	1.06e+01

ALIGNMENTS

RESULT 1
 ENTRY JF0082 #type complete
 TITLE GPI-linked receptor - mouse
 ALTERNATE_NAMES GPRalpha-3
 ORGANISM Mus musculus #common_name house mouse
 DATE 21-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1998

ACCESSIONS JF0082
 REFERENCE JF0082
 #authors Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
 #journal Blochem. Biophys. Res. Commun. (1998) 244:849-853
 #title Molecular cloning and expression analysis of GPRalpha-3
 #accession JF0082
 #molecule_type mRNA
 #residues 1-397 #label NOM

COMMENT ##cross-references DBRef:AB008833; NID:92627159; PID:92627160
 This protein plays a distinct role in cell survival and differentiation.
 KEYWORDS glycoprotein

FEATURE
 1-25 #domain signal sequence #status predicted #label S...
 380-397 #region hydrophobic
 92,145,306 #binding_site carbohydrate (Aan) (covalent) #status predicted

SUMMARY
 Query Match 23.2%; Score 777; DB 2; Length 397;
 Best local Similarity 38.5%; Pred. No. 4.61e-149;
 Matches 124; Conservative 74; Mismatches 99; Indels 25; Gaps 1

DB	41	CTQARRKCEANPACRAAYOHLSCTSSLRPLLESAMASDCLAEADLRNSSLDCNC	11
DB <td>36</td> <td>CVRANELCAAESNCSSRYTLRQCLAGRDNRNML--ANK--EQQAALVLEQSTPYNN</td> <td>11</td>	36	CVRANELCAAESNCSSRYTLRQCLAGRDNRNML--ANK--EQQAALVLEQSTPYNN	11
OY <td>101</td> <td>HRMRKQACLDIYVHPARSLGYEL-DVSPYEDITY--SKPKM-NL-S-K-L-N-L</td> <td>11</td>	101	HRMRKQACLDIYVHPARSLGYEL-DVSPYEDITY--SKPKM-NL-S-K-L-N-L	11
DB <td>92</td> <td>KRGMRKEQLQCLDIYSHLGLTEGE-EFEYASPYEPVTSRLDIFRLASIFGTFIDVAV</td> <td>11</td>	92	KRGMRKEQLQCLDIYSHLGLTEGE-EFEYASPYEPVTSRLDIFRLASIFGTFIDVAV	11
OY <td>153</td> <td>KPDSDLCTKFAKICTLHDKCDRLKRAYGACG-GI-----RCORHLCLOLRSEFFKAES</td> <td>20</td>	153	KPDSDLCTKFAKICTLHDKCDRLKRAYGACG-GI-----RCORHLCLOLRSEFFKAES	20
DB <td>151</td> <td>SKRSNRCDAACACNNDCKRLRSSYSICRREISPERCRRKCHALRAFPPRVSE</td> <td>210</td>	151	SKRSNRCDAACACNNDCKRLRSSYSICRREISPERCRRKCHALRAFPPRVSE	210
OY <td>208</td> <td>HAQGLLCPACBADAGCGERRNTIAPSCALPS-VTPNCLDLRSCFADPLCRSLMDFO</td> <td>266</td>	208	HAQGLLCPACBADAGCGERRNTIAPSCALPS-VTPNCLDLRSCFADPLCRSLMDFO	266
DB <td>211</td> <td>YVRLMFCSC-ODQA-CARRRQTIIPSCSYEDKRPNCPLDLRSLCRTHDLCRSLADPFH</td> <td>268</td>	211	YVRLMFCSC-ODQA-CARRRQTIIPSCSYEDKRPNCPLDLRSLCRTHDLCRSLADPFH	268

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Db 267 THEHPM-DLIGCATQOSR-CRATLGLIGRAMPNFISKVNTVALS--CTORGSGNIO 332
Y 269 ANRNASYKRTITSCPADNTOACLGASAGMIGFDMTPNYDSNPTIIVSPMCNCRGSGNME 328
Db 323 DECEQLERFSQNPCLVEAIIA 344
Y 329 ECECEKFLRDFTEPNCLRNAIQA 350

RESULT 2
ENTRY #type complete
TITLE gene 9 protein - human herpesvirus 3
ORGANISM #formal_name human herpesvirus 3; varicella-zoster virus
DATE 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change
14-Nov-1997

ACCESSIONS 127212
REFERENCE A27345
#authors J. Gen. Virol. (1986) 67:1759-1816
#journal The complete DNA sequence of varicella-zoster virus.
#title The complete DNA sequence of varicella-zoster virus.
#cross-references MUID:86306537
#accession 127212
#molecule_type DNA
#residues 1-302 #label DNA
#cross-references EMBL:X04370; NID:g55989; PID:g55998

GENETICS
#gene 9
CLASSIFICATION #superfamily varicella-zoster virus gene 9 protein
SUMMARY #length 302 #molecular_weight 32846 #checksum 3700

Query Match 3.1%; Score 102; DB 1; Length 302;
Best Local Similarity 28.6%; Pred. No. 1.33e-01;
Matches 16; Conservative 15; Mismatches 23; Indels 2; Gaps 2;

Db 9 LCRSNAVRKRTTPSYSGQRTARSRVYVGPDDSDSLG-YITTVGADSPSPYAD 63
Y 253 LCRTHLCRSRLADPHANCRASRYTITSCPADNTOACLGASAGMIGFDM-TPNYVD 307

RESULT 3
ENTRY #type complete
TITLE masking protein precursor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change
10-Sep-1997

ACCESSIONS A38261
REFERENCE A38261
#authors Tsujii, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8835-8839
#title Molecular cloning of the large subunit of transforming growth
factor type beta masking protein and expression of the mRNA
in various rat tissues.
#cross-references MUID:91062373
#accession A38261
#status preliminary
#molecule_type mRNA
#residues 1-1712 #label TSU
#cross-references GB:M55431; NID:g207285; PID:g207286
CLASSIFICATION #superfamily LDL receptor ligand-binding repeat homology
SUMMARY #length 1712 #molecular_weight 186598 #checksum 9047

Query Match 3.1%; Score 103; DB 2; Length 1712;
Best Local Similarity 34.9%; Pred. No. 9.37e-02;
Matches 15; Conservative 12; Mismatches 12; Indels 4; Gaps 4;

Db 1032 DECIOP-KVCH-NGSCNTEGYSWCSCHKGYPT-P-DHRHQ 1070
Y 155 NHCLDAARACLNNDCKLRSSYISICNRIESTPERCNRKCH 197

RESULT 4
ENTRY #type complete
TITLE response regulator homolog, aerial mycelium formation -

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[illegible]

Query Match 95.6%; Score 3196; DB 1; Length 463;
 Best Local Similarity 96.9%; Pred. No. 0.00e+00;
 Matches 438; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

DB 12 FLDETLASLSPSSPOGSEIHGMRPPVDCVRANELCAESNCSSRYRTLROCLAGDRNT 71
 : |||||
 OY 8 YPELTSLASPSLSGSELHGMRPVDCVRANELCAESNCSSRYRTLROCLAGDRNT 67
 DB 72 MLANKECOALAEVLOESPPLYDCRCRGMKKELOCIQIYWSIHGLTEGEFEYASPEPV 131
 : |||||
 OY 68 MLANKECOALAEVLOESPPLYDCRCRGMKKELOCIQIYWSIHGLTEGEFEYASPEPV 127
 DB 132 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKRLRSSYISICNREISP 191
 : |||||
 OY 128 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKRLRSSYISICNREISP 187
 DB 192 TERCNRKCHKALROFEDRVPSSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 251
 : |||||
 Y 188 TERCNRKCHKALROFEDRVPSSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 247
 DB 252 LDRSLCRTLDRSLADFHANCRASTRITISCPADNYOACLGSYAGMIGFDMTPNYVD 311
 : |||||
 OY 248 LDRSLCRTLDRSLADFHANCRASTRITISCPADNYOACLGSYAGMIGFDMTPNYVD 307
 DB 312 SNETGIVSPWCMCRGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNSPKGPTEG 371
 : |||||
 OY 308 SNETGIVSPWCMCRGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNSPKGPTEG 367
 DB 372 ATQAPRVKTPSLPDLSDSTSLGTSYITTCISIOEOGLKANKSKELSMCFELTTNISP 431
 : |||||
 OY 368 ATQAPRVKTPSLPDLSDSTSLGTSYITTCISIOEOGLKANKSKELSMCFELTTNISP 427
 DB 432 GSKKVIKLVGSGCARLSTALTALPLMLTLA 463
 : |||||
 OY 428 GSKKVIKLVGSGCARLSTALTALPLMLTLA 459

RESULT 2
 ID NTRR HUMAN STANDARD: PRT: 464 AA.
 AC 000451:
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNFR-BETA)
 GN GFR2 OR GDNFRB OR TRNR2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97325791.
 RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA HEUCKEROOTH R.O., KECK C.L., ZIMONIC D.B., POPESCU N.C.,
 RA JOHNSON E.M. JR., MILBRANDT J.:
 RA NEURON 18:793-802(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
 CC SPLICING IN BOTH BRAIN AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: AF002700; G2145080; -.
 DR MIM: 601956; -.
 KW RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 444 TGF-BETA RELATED NEUROTROPHIC FACTOR

FT PROPEP 445 464 RECEPTOR 2.
 FT CARBOHYD 52 52 HYDROPHOBIC. REMOVED DURING MATURATION
 FT CARBOHYD 357 357 (POTENTIAL).
 FT CARBOHYD 413 413 POTENTIAL.
 FT LIPID 444 444 POTENTIAL.
 FT VARSPLE 14 146 GPI-ANCHOR (POTENTIAL).
 SO SEQUENCE 464 AA. 51558 MW; 3C74BBEB CRC32;
 Query Match 93.3%; Score 3120; DB 1; Length 464;
 Best Local Similarity 94.0%; Pred. No. 0.00e+00;
 Matches 426; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

DB 12 FLDETLASLSPSSPOGSEIHGMRPPVDCVRANELCAESNCSSRYRTLROCLAGDRNT 71
 : |||||
 OY 8 YPELTSLASPSLSGSELHGMRPVDCVRANELCAESNCSSRYRTLROCLAGDRNT 67
 DB 72 MLANKECOALAEVLOESPPLYDCRCRGMKKELOCIQIYWSIHGLTEGEFEYASPEPV 131
 : |||||
 OY 68 MLANKECOALAEVLOESPPLYDCRCRGMKKELOCIQIYWSIHGLTEGEFEYASPEPV 127
 DB 132 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKRLRSSYISICNREISP 191
 : |||||
 OY 128 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKRLRSSYISICNREISP 187
 DB 192 TERCNRKCHKALROFEDRVPSSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 251
 : |||||
 OY 188 TERCNRKCHKALROFEDRVPSSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 247
 DB 252 LDRSLCRTLDRSLADFHANCRASTRITISCPADNYOACLGSYAGMIGFDMTPNYVD 311
 : |||||
 OY 248 LDRSLCRTLDRSLADFHANCRASTRITISCPADNYOACLGSYAGMIGFDMTPNYVD 307
 DB 312 SNETGIVSPWCMCRGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNSPKGPTEG 371
 : |||||
 OY 308 SNETGIVSPWCMCRGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNSPKGPTEG 367
 DB 372 ATQAPRVKTPSLPDLSDSTSLGTSYITTCISIOEOGLKANKSKELSMCFELTTNISP 431
 : |||||
 OY 368 ATQAPRVKTPSLPDLSDSTSLGTSYITTCISIOEOGLKANKSKELSMCFELTTNISP 427
 DB 432 GSKKVIKLVGSGCARLSTALTALPLMLTLA 464
 : |||||
 OY 428 GSKKVIKLVGSGCARLSTALTALPLMLTLA 460

RESULT 3
 ID NTRR CHICK STANDARD: PRT: 465 AA.
 AC 013157:
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GDNF
 DE RECEPTOR BETA) (GDNFR-BETA).
 GN GFR2 OR GDNFRB.
 OS GALUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RA BU-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
 RA ROSENTHAL A., CHINCHESTER M., BOCHMAN V.L., DAVIES A.M.:
 RA NATURE 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: U90542; G213805; -.
 DR RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFR1 OR GDNFRA OR TRNRI.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 DE NEURONIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-DORSAL ROOT GANGLION;
 RC WATARE K;
 RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: AB000800; G1816442; -
 DR MGD: MGI:1100842; GFR1.
 KM RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 430
 FT PROPEP 431 468
 FT DOMAIN 362 369
 FT CARBOHYD 59 59
 FT CARBOHYD 347 347
 FT CARBOHYD 406 406
 FT LIPID 430 430
 FT SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;
 SQ
 Query Match 46.18; Score 1541; DB 1; Length 468;
 Best Local Similarity 47.98; Pred. No. 0.00e+00;
 Matches 214; Conservative 103; Mismatches 116; Indels 14; Gaps 12;
 Db 16 LMSAEVSG-GDRLDVCAKADQCKECSCTKYRTLRQCVAGKESNLSGLEAKESCS 74
 Oy 22 LQSEELHGRPOVDVCAVRAELCAESNCSSRYRTLRQCLAGRRN-TM--LANK-ECOA 76
 Db 75 AEMALKOKSLNCRCKRKK 133
 Oy 77 ALEVLQESPLDYOCRCRKK 136
 b 134 AVPEITDVOOEYEHLSKNNCLDAKACNLDCTCKRYSAYITPTTNS-NEVCNRRKC 192
 Oy 137 LASFEGTGTDPVAVSTKSHNCDAKACNLDNCKLRSSYSISICNREISPTERCNRRKC 196
 Db 193 HKALRPFEPKPAKSHYGLFPCSCRVACTERRRQTIYVCSYEERENCLNLDSCYT 252
 Oy 197 HKALRPFEPKPAKSHYGLFPCSCRVACTERRRQTIYVCSYEERENCLNLDSCYT 256
 Db 253 NYICRSRLADFTNCPESRSYVNCLENYADCLAYSLGIGVTWTPNTIDSS-S-LSVA 310
 Oy 257 DHLCSRLADFTNCPESRSYVNCLENYADCLAYSLGIGVTWTPNTIDSS-S-LSVA 316
 Db 311 PWCDCNSGNDLEDCIKELNFKNDTCNKNAIOAFNGSDVTMMOPAPVOTTTATTTA 370
 Oy 317 PWCDCNSGNDLEDCIKELNFKNDTCNKNAIOAFNGSDVTMMOPAPVOTTTATTTA 375
 Db 371 PFKKKPLGPASSENIPIHYLPKCANIOAQCLKSNVSGSTHCLSDNDYKGLAGASS 430
 Oy 376 -KTPPLPDLDSDTS-LGTSVITCTSIQEOGLKANNSEKLSMCTELTITNISPSKVIY 433
 Db 431 HITTSMAPPSGGLSLPVVWFTALA 457
 Oy 434 KLNSSSSRRARLSAALTALPLMLT-LA 459
 RESULT 6

ID GDNF CHICK STANDARD: PRT: 469 AA.
 AC 013156;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFR1 OR GDNFRA.
 OS GALUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHA;
 OC GALIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
 RA ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
 RL NATURE 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: U90541; G2213803; -
 DR MGD: MGI:1100842; GFR1.
 KM RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 27
 FT CHAIN 28 430
 FT PROPEP 431 469
 FT DOMAIN 361 368
 FT CARBOHYD 62 62
 FT CARBOHYD 163 163
 FT CARBOHYD 346 346
 FT CARBOHYD 405 405
 FT LIPID 430 430
 FT SEQUENCE 469 AA; 52043 MW; C8D2A1C9 CRC32;
 SQ
 Query Match 45.48; Score 1519; DB 1; Length 469;
 Best Local Similarity 50.18; Pred. No. 0.00e+00;
 Matches 221; Conservative 99; Mismatches 96; Indels 25; Gaps 17;
 Db 29 RIDCVKASDQCKECSCTKYRTLRQCVAGKESNLSGLEAKESCS 88
 Oy 33 QVDCVRADELCAESNCSSRYRTLRQCLAGRD---RTMLANK-ECOALEVLQESPLY 87
 Db 89 NCRCRKK 144
 Oy 88 DCRCKRKK 147
 Db 145 PVLVS-KGNNCCLDAKACNLDNCKRFRSAYITPTTNS-NEICNKRCHALRFPDKY 202
 Oy 148 PAVSTKSHNCCLDAKACNLDNCKRFRSAYITPTTNS-NEICNKRCHALRFPDKY 207
 Db 203 PPKSHYGLFPCSCRVACTERRRQTIYVCSYEERENCLNLDSCYT 262
 Oy 208 PPKSHYGLFPCSCRVACTERRRQTIYVCSYEERENCLNLDSCYT 267
 Db 263 FTNCPESRSYVNCLENYADCLAYSLGIGVTWTPNTIDSS-S-LSVAPWCDCNSGND 320
 Oy 268 HANCRASRTTSCPADYQACLSYGIGVTWTPNTIDSS-S-LSVAPWCDCNSGND 327
 Db 321 IDECRKFLNFPQDWTCLNKAIOAFNGSDVTMMOPAPVOTTTATTTASRLKNTGNC 457
 Oy 328 EEECEKFLNFPQDWTCLNKAIOAFNGSDVTMMOPAPVOTTTATTTASRLKNTGNC 457
 Db 379 TTNEIPTHNDSPACANIOAQKRRKSNESYDTCLNENAIKGNTPGVGTS-HISSNN 457
 Oy 387 STS--LGT-SVITCTSIQEOGL-KANNSEKLSMCTE-LTITNISGSKKVIYLNKNS 457
 Db 438 FA-LPTSFYPTPLMLTIAL 457

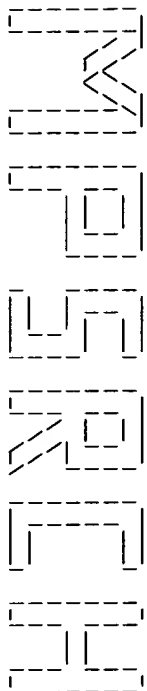
FT SITE 734 736 CLEAVAGE (POTENTIAL).
FT SITE 1575 1577 CLEAVAGE (POTENTIAL).
FT PROPEP 1578 1712 POTENTIAL.
FT DOMAIN 181 213 EGF-LIKE 1.
FT DOMAIN 391 423 EGF-LIKE 2.
FT REPEAT 351 604 INTERNAL REPEAT 1.
FT DOMAIN 618 658 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 671 721 INTERNAL REPEAT 2.
FT DOMAIN 865 906 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 907 948 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 949 989 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 990 1029 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1030 1070 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1071 1111 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1112 1152 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1153 1193 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1235 1235 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1236 1277 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1278 1330 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 1340 1392 INTERNAL REPEAT 3.
FT DOMAIN 1415 1457 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1458 1498 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 1577 1588 INTERNAL REPEAT 4.
FT DOMAIN 1612 1652 EGF-LIKE 17.
FT DOMAIN 1653 1697 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 185 195 BY SIMILARITY.
FT DISULFID 189 201 BY SIMILARITY.
FT DISULFID 203 212 BY SIMILARITY.
FT DISULFID 395 405 BY SIMILARITY.
FT DISULFID 399 411 BY SIMILARITY.
FT DISULFID 413 422 BY SIMILARITY.
FT DISULFID 622 633 BY SIMILARITY.
FT DISULFID 628 642 BY SIMILARITY.
FT DISULFID 644 657 BY SIMILARITY.
FT DISULFID 869 881 BY SIMILARITY.
FT DISULFID 876 890 BY SIMILARITY.
FT DISULFID 892 905 BY SIMILARITY.
FT DISULFID 911 923 BY SIMILARITY.
FT DISULFID 918 932 BY SIMILARITY.
FT DISULFID 934 947 BY SIMILARITY.
FT DISULFID 953 964 BY SIMILARITY.
FT DISULFID 959 973 BY SIMILARITY.
FT DISULFID 976 988 BY SIMILARITY.
FT DISULFID 994 1005 BY SIMILARITY.
FT DISULFID 1000 1014 BY SIMILARITY.
FT DISULFID 1017 1028 BY SIMILARITY.
FT DISULFID 1034 1045 BY SIMILARITY.
FT DISULFID 1040 1054 BY SIMILARITY.
FT DISULFID 1056 1069 BY SIMILARITY.
FT DISULFID 1075 1086 BY SIMILARITY.
FT DISULFID 1081 1095 BY SIMILARITY.
FT DISULFID 1097 1110 BY SIMILARITY.
FT DISULFID 1116 1127 BY SIMILARITY.
FT DISULFID 1122 1136 BY SIMILARITY.
FT DISULFID 1138 1151 BY SIMILARITY.
FT DISULFID 1157 1169 BY SIMILARITY.
FT DISULFID 1164 1178 BY SIMILARITY.
FT DISULFID 1180 1192 BY SIMILARITY.
FT DISULFID 1198 1210 BY SIMILARITY.
FT DISULFID 1204 1219 BY SIMILARITY.
FT DISULFID 1221 1234 BY SIMILARITY.
FT DISULFID 1240 1252 BY SIMILARITY.
FT DISULFID 1246 1261 BY SIMILARITY.
FT DISULFID 1263 1276 BY SIMILARITY.
FT DISULFID 1282 1294 BY SIMILARITY.
FT DISULFID 1289 1303 BY SIMILARITY.
FT DISULFID 1305 1319 BY SIMILARITY.
FT DISULFID 1419 1432 BY SIMILARITY.
FT DISULFID 1427 1441 BY SIMILARITY.
FT DISULFID 1443 1456 BY SIMILARITY.
FT DISULFID 1462 1473 BY SIMILARITY.
FT DISULFID 1468 1482 BY SIMILARITY.
FT DISULFID 1484 1497 BY SIMILARITY.

FT DISULFID 1616 1627 BY SIMILARITY.
FT DISULFID 1622 1636 BY SIMILARITY.
FT DISULFID 1638 1651 BY SIMILARITY.
FT DISULFID 1657 1672 BY SIMILARITY.
FT DISULFID 1677 1681 BY SIMILARITY.
FT DISULFID 1683 1696 BY SIMILARITY.
FT CARBOHYD 339 339 POTENTIAL.
FT CARBOHYD 370 370 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 612 612 POTENTIAL.
FT CARBOHYD 1042 1042 POTENTIAL.
FT CARBOHYD 1242 1242 POTENTIAL.
FT CARBOHYD 1357 1357 POTENTIAL.
SQ SEQUENCE 1712 AA; 186598 MW; 7C924DB1 CRC32;

Query Match 3.1%; Score 103; DB 1; Length 1712;
Best Local Similarity 34.9%; Pred. No. 1,486-02;
Matches 15; Conservative 12; Mismatches 12; Indels 4; Gaps 4;

DB 1032 DECLAP-KVCF-NGSCTNLESGYSCHEKGYSP-P-DHRGQ 1070
OY 155 NHCLDAARACNLNDCKRTRSSYSICNREISPERCNRRCH 197

RESULT 10 STANDARD; PRT: 354 AA.
ID NOV-MOUSE
AC 064299;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
GN NOV.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV. AND ICR. TISSUE-BRAIN;
RA SNAITH M.R., NARAJAN D., TAYLOR L.B., CHOI C.P., MARTINERIE C.,
PERBAL B., SCHOFIELD P.N., BOUTLER C.A.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 96204003.
RA MARTINERIE C., CHEVALIER G., RAUSCHER F.J. III, PERBAL B.;
RL ONCOGENE 12:1479-1492(1996).
CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
GROWTH REGULATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN FAMILY. CEF-10/CTRG1/CTRG/ETSP-12/NOV PROTEIN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 WFC DOMAIN.
CC EMBL; X97863; E1811580; -;
DR EMBL; Y09257; E281106; -;
DR EMBL; X96585; E228599; -;
DR MGD; MGI:109185; NOV.
DR PROSITE; PS00222; IGF-BINDING; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01208; WFC; 1.
KW PROTO-ONCOGENE; GROWTH FACTOR BINDING; SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 354 NOV PROTEIN HOMOLOG.
FT DOMAIN 102 168 WFC.
FT DOMAIN 261 335 CTCK.
FT DISULFID 261 298 BY SIMILARITY.
FT DISULFID 278 312 BY SIMILARITY.
FT DISULFID 289 328 BY SIMILARITY.
FT DISULFID 292 330 BY SIMILARITY.
FT DISULFID 297 334 BY SIMILARITY.
FT CARBOHYD 91 91 POTENTIAL.
FT CARBOHYD 277 277 POTENTIAL.



(TM)

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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 14:35:04 1999; Maspar time 271.20 Seconds 852.349 Million cell updates/sec

Tabular output not generated.

Title: >US-08-866-354-41
Description: (1-1699) from US08866354.seq
Perfect Score: 1699
N.A. Sequence: 1 GCGCGCGCGCGACGACGACG.....CCACCGCTCGACGCGCGCGC 1699
Comp: CGCGCGCGCGACGCTGCTGCG.....GGTTGGACGCTGCGCGCGCGC

Scoring table: TABLE default
Gap 6

Nmatch SMD : Dbase 0; Query 0

Searched: 188442 segs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

n-gene32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.447; Variance 5.382; scale 1.755

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1123	66.1	1878	39	V00256	Mouse Ret ligand retl
2	1120	65.9	1889	39	V00249	Mouse Ret ligand retl
3	805	47.4	1699	39	V00251	Human Ret ligand retl
4	695	40.9	1271	39	V00250	Human Ret ligand retl
5	43	2.5	91	9	Q51746	Oligonucleotide probe
6	41	2.4	91	9	Q51746	Oligonucleotide probe
7	40	2.4	204	1	N81164	Base substituted E.co
8	38	2.2	114	12	Q70468	Generic DNA sequence
9	38	2.2	114	12	Q70466	Generic DNA sequence
10	37	2.2	204	1	N81164	Base substituted E.co
11	37	2.2	1888	39	V00248	Human Ret ligand retl
12	36	2.1	114	12	Q70469	Generic DNA sequence
13	36	2.1	114	12	Q70466	Generic DNA sequence

14	34	2.0	114	12	Q70465	Generic DNA sequence
15	34	2.0	114	12	Q70467	Generic DNA sequence
16	34	2.0	114	12	Q70467	Generic DNA sequence
17	34	2.0	114	12	Q70468	Generic DNA sequence
18	34	2.0	114	12	Q70465	Generic DNA sequence
19	32	1.9	114	12	Q70470	Generic DNA sequence
20	32	1.9	114	12	Q70469	Generic DNA sequence
21	33	1.9	172	32	T76363	Human interleukin 8 a
22	33	1.9	178	32	T76405	Human endothelin-1 an
23	32	1.9	178	32	T76405	Human endothelin-1 an
24	32	1.9	1223	39	V00246	Human Ret ligand retl
25	32	1.9	1682	39	V00247	Human Ret ligand retl
26	32	1.9	2568	38	T88419	Human glial cell line
27	31	1.8	114	12	Q70473	Generic DNA sequence
28	31	1.8	114	12	Q70472	Generic DNA sequence
29	30	1.8	114	12	Q70471	Generic DNA sequence
30	30	1.8	114	12	Q70470	Generic DNA sequence
31	30	1.8	114	12	Q70472	Generic DNA sequence
32	30	1.8	565	6	Q35072	HCV envelope region n
33	30	1.8	3871	2	N71302	HSV-1 gB and surround
34	29	1.7	130	32	T76152	Human vascular cell a
35	29	1.7	172	32	T76363	Human interleukin 8 a
36	29	1.7	250	32	T76438	Substance P antisense
37	27	1.6	114	12	Q70471	Generic DNA sequence
38	27	1.6	125	32	T76423	Human endothelin ERA
39	27	1.6	128	32	T76233	Human IL6 antisense o
40	28	1.6	168	32	T76270	Human MDMCF antisense
41	28	1.6	190	32	T76452	Clymase antisense o11
42	28	1.6	190	32	T76452	Clymase antisense o11
43	27	1.6	264	32	T76445	Substance P receptor
44	28	1.6	379	32	T76527	Inducible nitric oxid
45	27	1.6	453	37	T84979	Human Est-derived seq

ALIGNMENTS

RESULT 1	V00256 standard; cDNA; 1878 BP.
ID	V00256:
AC	21-MAY-1998 (first entry)
DE	Mouse Ret ligand retl3 cDNA partial clone (EST AA50083).
KW	Ret ligand; Retl; Retl3; receptor; signal transduction; mouse;
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;
KW	Kidney transplant; toxic injury; hypoxic injury;
KW	neurodegeneration; motor neuron disease; multiple sclerosis;
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW	cerebral palsy; Lyme disease; muscular dystrophy;
KW	myasthenia gravis; tumour; therapy; ss.
OS	Mus musculus.
FH	Key
FT	Location/Qualifiers
FT	205..1245
FT	CDS
FT	/*tag a
PD	NO9744356-A2.
PN	27-NOV-1997.
PF	07-MAY-1997: U07726.
PR	10-APR-1997: US-017427.
PR	08-MAY-1996: US-017427.
PR	07-JUN-1996: US-019300.
PR	16-JUL-1996: US-021859.
PR	(BioJ) BIOGEN INC.
PI	Cate RL; Hession C; Sanicola-Nadel M;
PI	WPI: 98-018431/02.
DR	P-PSDB: W37465.
PT	New nucleic acid encoding ret receptor ligands and related proteins
PT	- vectors, transformed cells and antibodies, used for promoting cell
PT	growth and improving survival of injured cells, especially renal or
PT	nerve cells
PS	Disclosure: page 71-73: 113pp: English.
CC	This sequence comprises EST AA50083, identified as a partial cDNA
CC	for mouse Ret ligand (Retl) Retl3 (see W37465), by screening of
CC	an EST database with rat Retl1 (see W37457). A full-length
CC	mouse retl3 cDNA clone (see V00249) was obtained by combining

CC AA050083 with a clone obtained by 5'RACE. Rat. mouse and human retL2 and retL3 cDNA sequences (see V00245-1) and CC encoded polypeptides (see W37457-3) are claimed and can be used CC in methods for promoting cell growth and improving survival of CC cells, especially renal or neural cells.

SO Sequence 1878 bp. 389 A. 575 C. 478 G. 436 T.

Query Match	66.18;	Score 1123;	DB 39;	Length 1878;
Best Local Similarity	91.98;	Pred. No. 0.00e+00;		
Matches 1248;	Conservative	0;	Mismatches 107;	Indels 3;
				Gaps 2;

[illegible]

Oy	915	CAGATGCTGGGGCAGATACCTGGGGCGTAATTGGGACATGGCATATGACCCCAAACTTATCAG	974
Db	960	caaggccaacactactcgtctgccttaagctcgacctcgcgagccagcgcgcaactcaagga	10191
Oy	975	CAAGGTCAACACTACTGTTCCTTAGGCTGACTCCGAGGCAATGGCAACTTCACAGA	10334
Db	1020	cgagctggaacaagctcgtgaaagtcctctctccagaagccctcctcctgtagagcatctgc	10797
Oy	1035	CGAGTGTGAACAGCTGGGAAAGTCCTTCTCCAGAACCCCTGCTCATAGAGGACCATTC	10944
Db	1080	agctcaagaatgcgtttccacagaagaagctctctccagaagctcgcgagactactcttctc	11380
Oy	1095	GGCTAAATATCGTTCCTCCACGACACTCTTCTCCCGAGACTGGGGGACTACTACTTTTC	11544
Db	1140	agctgtcagaacagcagaagacgaaccctcctctgagactcgcagcccaagctaccactctc	11989
Oy	1155	TGTATGACACAGCAGACAGCAGCCCTCTGTGAAGCCCCAGCTACACCGTCT	12144
Db	1200	ttctcttcacatctctccctctgtattctgtctgagagacctctgtatctcgggctctctag	12589
Oy	1215	GTCCTTTTATCTTACTTACTTGTGTTGCTGAGACCCCTCTGTACTGTGGGTCTCCCTAG	12747
Db	1260	ggtccctctgcctctccacacacccacagactatctgacagctcgtgctggtgagagaactc	13191
Oy	1275	GGTCTTTGTGCTCTCTCCACACACCCAGACCGACTTGACGCTGTGATGGGAGGAAAT	13344
Db	1320	gcacagcctgtgagaagaagcagcgcgtgtctacacagca	1357
Oy	1335	GCTGGCCTCTGGAGAAGATGCAACAGGCTACATCTGCA	1372

RESULT 2

ID	V00249	standard: cDNA; 1889 BP.
AC	V00249	
DT	21-MAR-1998	(first entry)
DE	Mouse Ret ligand retL3 cDNA.	
KW	Ret ligand; RetL3; RetL3; receptor; signal transduction; mouse;	
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;	
KW	kidney transplant; toxic injury; hypoxic injury;	
KW	neurodegeneration; motor neurone disease; multiple sclerosis;	
KW	infection; meningitis; myelopathy; Creutzfeldt-Jacob disease;	
KW	cranial nerve injury; spinal cord injury; Down's syndrome;	
KW	cerebral palsy; Lyme disease; muscular dystrophy;	
KW	myasthenia gravis; tumour; therapy; ss.	
OS	Mus musculus.	
FH		
FT	Key	Location/Qualifiers
FT	CDS	41..1234
PN		/tag= a
PD	MO9744356-A2.	
PF	27-NOV-1997.	
PE	07-MAY-1997; U07726.	
PR	10-APR-1997; US-0174427.	
PR	08-MAY-1996; US-017427.	
PR	07-JUN-1996; US-019300.	
PR	16-JUL-1996; US-021859.	
PA	BiOcl) BIOGEN INC.	
PI	Cate RL, Hession C, Santicola-Nadel M;	
DR	WPI: 98-018431/02.	
PT	P-PSDB; W37461.	
PT	New nucleic acid encoding ret receptor ligands and related prot-	
PT	- vectors, transfected cells and antibodies, used for promoting cell	
PT	growth and improving survival of injured cells, especially renal o	
PT	nerve cells	
CC	claim 1: Page 75-77; 113pp; English.	
CC	This sequence comprises cDNA coding for mouse Ret ligand (RetL)	
CC	RetL3 (see W37461), a key component of the Ret signaling pathway.	
CC	It was deduced from a partial clone (see V00256) obtained from	
CC	from an EST database search with rat RetL1 (see W37457) and from	
CC	a clone obtained by 5' RACE. Rat and human retL1, and human retL2	
CC	and retL3 DNA sequences are also claimed (see V00245-48 and	
CC	V00250-51). Vectors containing retL3 DNA and prokaryotic or	
CC	eukaryotic host cells transformed or transfected with these vectors	
CC	are claimed, as well as a method for production of RetL3, its	

CC This sequence comprises a partial cDNA clone, designated GJ28,
CC for human Ret ligand (Ret), Ret3 (see W37463), a key component of
CC the Ret signalling pathway. It was isolated from a human adult
CC heart cDNA library using a probe derived from a mouse Ret3 partial
CC cDNA (see V00255). A full-length sequence (see V00251) for human
CC Ret3 cDNA has also been obtained, as well as rat and human Ret1,
CC human Ret2 and mouse Ret3 sequences (see V00245-51). Vectors
CC containing Ret3 DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of Ret3, its soluble variants and
CC fusion proteins with a toxin, immunizable compound or radionuclide,
CC Ret3, optionally when expressed from vectors *in vivo*, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving the
CC peripheral nervous system (Lyme disease, muscular dystrophy and
CC myasthenia gravis). Fusion proteins are used to deliver toxins
CC etc. to Ret-expressing cells, especially tumours.

Query Match	40.9%;	Score 695;	DB 39;	Length 1271;
Best Local Similarity	83.9%;	Pred. No. 0.00e+00;		
Matches	866;	Conservative	0;	Mismatches 165; Indels 1; Gaps 1

Db	15	caaccctcaactaagbaaagcgtctcttgataagctcatgatgtgcacccagcgcatgaagAAC	74
Oy	326	CACAGCAACTAGGAGAACGCTCTCTCATAGACTCAAGGTGCGACCGCGCATGAAGCAC	385
Db	75	aggttcctctgctcttgacatctcatcttgagaccgtctcaacgcttgcgcgcagcctctgtaacatg	134
Oy	386	AAGCTACTGTGTGGACATTATTATGGACCGTTCAACCGTGTCCGAAGCCTTGTTGACTACG	445
Db	135	agcttgatgtctctccctcatgaagacacagtgcacagcaaacctctgaaaaatgaattca	194
Oy	446	AGTTGGAGCTGTACACCCCTATAGAGACAGAGACAGAAACCTGTGAAAATGATCTCA	505
Db	195	gcaaacctgaacatgtctcaaacacagactcagacccctcgtcctaagtttgcctatgtctgta	254
Oy	506	GCAAGCTAGCATGTCTCAACACCACTCCGACTCTGCTCTAAATTTCATGCTGTGTA	565
Db	235	ctctcaatgaacagatgtgacccggtctgcgcaagagctcaacggaagcgctgtcccgcgcc	314
Oy	556	CTCTTAACGACAAAGTGGACCGGCTCCGAAAGGCTAAGGGAGGCGTCAAGGATCC	625
Db	315	actgtccaaagcgcaagctctgcctcaaggcagcgctcactttcttgaaaaagccgcgagc	374
Oy	626	GCTGCGACCGCACCTCTGCTTACGTCAAGCTGACGTGCGCTCTCTTTTGAGAAAGCGGCAAGT	685
Db	375	cccaacgcgcagagccctgtactgtgcccattgtgcccacagacagccgggctgcgcggagc	434
Oy	686	CCCAAGCTCAGAGCGCTGCTGTGCTGTCCCTGTGCACCCGAAAGATGCGGGCTGTGGGAGC	745
Db	435	gccggcgcaacaacatgcgcccacacatgcgcgtctgcgctgtgcccccaactgccttg	494
Oy	746	GCGCGCGCAACACATCGCCCCCAAGTTGCGGCTTCCCTCTGTGTGGCCCCCAACTGCTTAG	805
Db	495	agcttcgcgcgcctctgcctcttcctgcgcgcgcgttttcagatgaacgcctgigtatctcaga	554
Oy	806	ATCTTCGGAGCTTCTGCCGTGGCGACCCCTCTGTGCAAGTACAGCCTGTATGGACTTCCAGA	865
Db	555	cccaactgcacatcccatggacatctcattaggaactgtgtgcacaagcagctccagaatgttac	614
Oy	866	CCCACTGCACACCTTATGACATCTCGGAGCTTGTGCAACTGACAGACGACGATGTCTGC	925
Db	615	gaagctactcgggagctgtgttggaactgtcatgaccccccaacttgttaagaatgttaaa	674
Oy	926	GGGCAATTACTGGGCTAATTATGGACTGTGCATGACCCCAAACTTATCATGCAAGGTACAA	985

Db	675	ccagatgtgccttaagcttaaccttgcgcggagcagtggaaccttgcaggaaagagtgtaaa	734
Oy	986	CTACTGTTGCTTTAGGCTGTACTGCTGCCGAGCGACAGTGGCACTGCAGACGAGTGTGAC	1045
Db	735	tgcttgaagaggttcttcttcccaaaccccttgctctcaggaagcatalgcagctaaagatgc	794
Oy	1046	AGCTGAAAAAGTCCCTTCTTCCAGAACCCCTGCGCTCATGAGGCGCATTTGGGCTAAATATGC	1105
Db	795	gttttcacagcacaacttcttcccaagagacttgcacaaaccttacccttgcgtgtgaatgcac	854
Oy	1106	GTTTCCACAGACAACCTTTCTCCAGAGCTGGGCGGACCTCACTTTTCTGTGAATGACGC	1165
Db	855	accagaaatgaaaaaccttgcgtgtgaagccaaagccctgggtgcacctctcttctctctcaga	914
Oy	1166	AGCGAAMACAGACGCCCTGCTCTGTAGGCCCCCAAGCTCAAGCTTACCCGTTCTGTCTTTCTTCA	1225
Db	915	cgcctcccttgatcttgcctctctcagcctatgtaagcttgagcttcccaacagagccctctctc	973
Oy	1226	TGCTTACTTGATGTCTGCTGACAGCCCTGTGGTAATGGGCTCCGTCAGAGGTCCTTTGTC	1285
Db	974	cccttcacacacaccccaaggttgactttgcagcctcccaaaaggggtgaagaaagacacgaagag	1033
Oy	1286	CTCTCCACACACACCCACACCCGACCTGTGAGCTGTGATGGAGAGAAAATGCTGGGCTCTG	1345
Db	1034	gaaggaagtgca	1045
Oy	1346	GAGAGAGATGCA	1357

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RESULT      5
AC           Q51746 standard; cDNA; 91 BP.
ID           Q51746;
DT           31-MAY-1994 (first entry)
DE           Oligonucleotide probe MK14-A
KW           Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KM           ss.
OS           Synthetic.
PN           EP-571911-A.
PR           26-MAY-1992; US-889651.
PA           (BECT ) BECTON DICKINSON CO.
PI           Shank DD; Spears PA;
PT           WPI: 93-37884/48.
PT           New oligo:nucleotide probes specific for Mycobacteria - used for
PT           detection and amplification of Mycobacteria nucleic acid in
PT           samples
PS           Claim 3; Page 14; 23pp; English.
CC           Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC           (051735). It hybridized to all spp. of mycobacteria tested, but
CC           cross reacted to a few non-mycobacterial spp. The probe may
CC           be useful as an initial screen for mycobacterial infection.
CC           See also Q51735-45 and Q51747-59.
SQ           Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match          2.5%; Score 43; DB 9; Length 91;
Best Local Similarity 3.8%; Pred. No. 2,20e+11;
Matches 2; Conservative 46; Mismatches 5; Indels 0;

Db      8 gggagshyyvvvhhshhvhhvvhhvvvvvvhhvvhhvvhhvyhvasv 50
        ||:::||||| : ::::::::::::::::::::
Cp      929 GCCGCGAGACATCTGCAGTCTCAAGTTGCACAGTCGCCAGATGTCATTAGG 877

RESULT      6
ID           Q51746 standard; cDNA; 91 BP.
AC           Q51746;
DT           31-MAY-1994 (first entry)
DE           Oligonucleotide probe MK14-A
KW           Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KM           ss.
OS           Synthetic.
PN           EP-571911-A.
```

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PD 01-DEC-1993.
PD 24-MAY-1993; 108325.
PR 26-MAY-1992; US-889651.
PR (BECT ) BECTON DICKINSON CO.
PI Shank DD, Spears PA.
PI WPI; 93-378844/48.
PT New oligo:nucleotide probes specific for Mycobacteria - used for
PT detection and amplification of Mycobacteria nucleic acid in
PS samples
PS Claim 3; Page 14; 23pp; English.
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
CC cross reacted to a few non-mycobacterial spp. The probe may
CC be useful as an initial screen for mycobacterial infection.
CC See also Q51735-45 and Q51747-59.
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 2.4%; Score 41; DB 9; Length 91;
Best Local Similarity 2.0%; Pred. No. 3,54e-10;
Matches 1; Conservative 44; Mismatches 4; Indels 0; Gaps 0;

Db 13 vhsyvvhvshhshvhhvhhvshvvvhhvhhvhhvhhvhyhvsvc 61
Oy 837 GTCGAGATCAGCGCTGATGACTTCCACACCCACACCTATGAC 885
::: ::::: : : ::::: ::::: ::::: ::::: ::::: ::::: :::::

RESULT 7
ID N81164 standard; DNA: 204 BP.
AC N81164;
MT 08-NOV-1990 (first entry)
DE Base substituted E.coli beta-galactosidase alpha-fragment.
KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
OS Escherichia coli.
FH Key Location/Qualifiers
FT misc_feature 19..69
FT /tag= a
FT /function= multiple cloning site
FT primer_bind 187..204
FT /tag= b

EP-285123-A.
PD 05-MAY-1988.
PR 30-MAR-1988; 105163.
PR 03-APR-1987; US-034819.
PA (SUSO) SUOMEN SOKERI OY.
PI Lehtovaara P, Knowles J, Kotivula A, Bamford J, Reinikainen T;
PI WPI; 88-279927/40.
PT Introducing random point mutations into nucleic acids -
PT by prepn of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.
PS Disclosure; P: English.
CC Random point mutations were introduced into the alpha fragment of
CC E.coli beta galactosidase. The wild type sequence was obtained as a
CC single stranded template and an oligonucleotide was hybridised to
CC it to generate a popn of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC reverse transcriptase. Nucleotides are misincorporated by the
CC transcriptase and the molecules are completed to forms that can be
CC amplified and then expressed in a suitable host-vector system.
CC The sequence covers all 176 diff base substitutions, most of which
CC occurred singularly in any given mutant.
SQ See also P80573.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match 2.4%; Score 40; DB 1; Length 204;
Best Local Similarity 11.6%; Pred. No. 1.40e-09;
Matches 11; Conservative 52; Mismatches 31; Indels 1; Gaps 1;

Db 95 rrmhbnvrydnyrsdaa-awyccyrysvkdcgcyneahdhvvybbvbnvnmhncnc 153
Oy 1410 AGGCGCTGACCGCTGAGATTCGTCGAGCGGCCACAGCTTTCAACCTCTCTACTTACTCT 1469
::: ::::: : : ::::: ::::: ::::: ::::: ::::: ::::: :::::
::: ::::: : : ::::: ::::: ::::: ::::: ::::: ::::: :::::
::: ::::: : : ::::: ::::: ::::: ::::: ::::: ::::: :::::

Db 154 ccbmhvchvbnhbnhvnwavyzhdariddvhncv 188

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QY      1470 GCTTGGGCGTCGCTCCCTAGACCTGTACTCA 1504
          ||:::| |:::|||||
RESULT 8
ID       Q70468 standard; DNA; 114 BP.
AC       Q70468;
DT       05-APR-1995 (first entry)
DE       Generic DNA sequence to generate a random TSAR peptide library.
KW       TSARs: totally synthetic affinity reagent; synthetic; binding domain;
        effector domain; concatenated heterofunctional protein; linker;
        direct; rapid; detection; screening; treatment; generic; ss.
OS       Synthetic.
FH
FT       misc-feature           location/Qualifiers
FT                                     55..60
FT                                     /*tag= a
FT                                     /note= "this sequence represents 'z'; z can be a
FT                                     sequence of 6, 9 or 12 nucleotides (see
FT                                     comments)"
PN
PR       MO9418318-A.
PE       18-AUG-1994.
PF       01-FEB-1994; U00977.
PR       01-FEB-1993; US-013416.
PR       30-DEC-1993; US-176500.
PA       31-JAN-1994; US-189331.
PR       (UNKN-) DMV NORTH CAROLINA.
PI       Fowlkes DM, Kay BK;
DR       WPI; 94-279739/34.
PT       P-PDB; R65154.
PT       Identifying proteins or peptide(s) which bind a ligand - by
PT       screening a recombinant vector library expressing fusion proteins
PT       comprising a binding domain and an effector domain
PS       Disclosure; Page 35; 25pp; English.
CC       Q70468 is a generic DNA sequence used to generate random TSAR (Totally
CC       Synthetic Affinity Reagents) peptides. This generic formula can also be
CC       represented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X
CC       and Y are flanking restriction sites (X is not the same as Y) that are
CC       not specified further. Other generic sequences are shown in Q70466-68.
CC       Other specific peptides generated by these generic sequences are shown in
CC       CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC       comprising at least two functional regions - a binding domain with
CC       affinity for a ligand and a second effector peptide portion that is
CC       chemically or biologically active. They may further comprise a linker
CC       peptide between the 2 domains. The oligonucleotides are also designed so
CC       that the expressed peptide contains 2 or 4 cysteine residues positioned
CC       in, or flanking, the unpredicted or variant residues. These residues
CC       confer some degree of conformational rigidity to the peptides. The TSARs
CC       or compms, comprising a TSAR binding domain can be used in vivo to
CC       deliver a chemically or biologically active moiety, eg. metal ion,
CC       radiolotope, peptide, toxin or enzyme, to the specific target cell.
CC       cell. They can also replace the function of macromolecules, e.g.,
CC       monoclonal or polyclonal antibodies and therefore circumvent the need
CC       for complex methods of hybridoma formation or in vivo antibody
CC       production. The TSARs are easily characterised and have designed .....
CC       allowing direct and rapid detection in a screening process.
SQ       Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

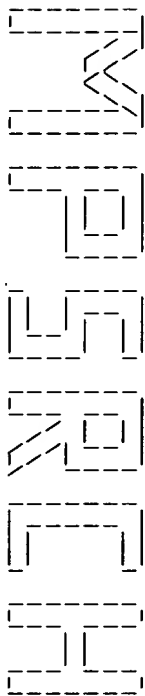
Query Match      2.2%; Score 38; DB 12; Length 114;
Best Local Similarity 5.4%; Pred. No. 2,14e+08;
Matches 6; Conservative 33; Mismatches 73; Indels 0; Gaps 0;

Db 3 bnnbnbnbnbnbnbnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnnnnnn 62
QY 625 CGTGCGAGGCCACCTGTGCTAGGTACGCTGCGCCTCTCTTCGAGAAGCGCGCAGAG 604

Db 63 bnnbnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 114
QY 685 TCCACAGCTCAGGGCCTGCTGTGTGCTCTGTGATGCACCAGAAATGCGGCT 736

RESULT 9
ID       Q70466 standard; DNA; 114 BP.
AC       Q70466;

```



(TM)

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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:37:58 1999; MasPar time 14.37 Seconds

Tabular output not generated. 447.095 Million cell updates/sec

Title: >US-08-866-354-42
Description: (1-397) from US08866354.pep
Perfect Score: 2962

Sequence: 1 MGLSRSPRPPLVILLVLS.....LRPVLSFILLITLITLW 397

Scoring table:
PAM 150
Gap 11

Searched: 131922 segs, 16180660 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

a-gene32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.465; Variance 144.588; scale 0.238

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2781	93.9	397	28	M37461 Mouse Ret ligand RetL	4.98e-267
2	2386	79.9	400	28	M37463 Mouse Ret ligand RetL	1.42e-224
3	2347	79.2	346	28	M37465 Mouse Ret ligand RetL	1.24e-222
4	1977	66.7	315	28	M37462 Human Ret ligand RetL	7.26e-185
5	759	25.6	464	28	M37460 Human Ret ligand RetL	9.15e-62
6	744	25.1	460	28	M37459 Human Ret ligand RetL	2.83e-60
7	708	23.9	465	28	M35333 Human Ret ligand RetL	1.06e-56
8	695	23.5	468	28	M37457 Rat Ret ligand RetL	2.05e-55
9	685	23.5	468	27	M27327 Rat Ret ligand RetL	2.05e-55
10	655	23.5	468	28	M35334 Rat Ret ligand RetL	2.05e-55
11	546	18.4	346	28	M37458 Human Ret ligand RetL	6.48e-41
12	102	3.4	459	2	R08329 Human Ret ligand RetL	5.99e+00
13	97	3.3	904	1	R05619 Human Ret ligand RetL	1.51e+01
14	91	3.1	144	20	M03523 Human Ret ligand RetL	4.10e+01
15	93	3.1	146	18	R99489 Human Ret ligand RetL	2.95e+01
16	93	3.1	148	18	R99496 Human Ret ligand RetL	2.95e+01
17	91	3.1	308	21	M10667 Human Ret ligand RetL	4.10e+01
18	91	3.1	308	21	M10672 Human Ret ligand RetL	4.10e+01

19	91	3.1	308	21	M10668 Human TGF-beta-like c	4.10e+01
20	91	3.1	308	21	M10671 Human TGF-beta-like c	4.10e+01
21	91	3.1	308	21	M10666 Human TGF-beta-like c	4.10e+01
22	91	3.1	308	21	M10673 Human TGF-beta-like c	4.10e+01
23	93	3.1	367	26	M29878 Lysophosphatidic acid	2.95e+01
24	92	3.1	1810	16	R94563 Chicken cytolactin	3.48e+01
25	91	3.1	2351	3	P60741 Sequence of human fac	4.10e+01
26	90	3.0	64	16	R86894 Prepro-LAP #2	4.82e+01
27	90	3.0	65	16	R86895 Prepro-LAP #2	4.82e+01
28	88	3.0	100	18	M00075 Ob protein fragment #	6.67e+01
29	88	3.0	100	18	M00065 C-terminally truncate	6.67e+01
30	88	3.0	119	18	M00067 C-terminally truncate	6.67e+01
31	88	3.0	128	18	M00069 C-terminally truncate	6.67e+01
32	88	3.0	128	20	M01404 Generic ob protein, 1	6.67e+01
33	88	3.0	141	18	M00105 N-terminally truncate	6.67e+01
34	88	3.0	141	18	M00050 Generic ob protein, 1	6.67e+01
35	88	3.0	146	18	R99497 N-terminally truncate	6.67e+01
36	88	3.0	146	18	R99498 Generic ob protein (T	6.67e+01
37	90	3.0	308	16	R84710 Human embryonal lung	4.82e+01
38	90	3.0	308	21	M10669 Human TGF-beta-like c	4.82e+01
39	90	3.0	308	16	R77097 Human TGF-beta-like c	4.82e+01
40	90	3.0	308	21	M10670 Human TGF-beta-like c	4.82e+01
41	90	3.0	308	21	M10662 Human TGF-beta-like c	4.82e+01
42	90	3.0	318	21	M10663 Human TGF-beta-like c	4.82e+01
43	90	3.0	371	15	R75642 Bovine conglutinin	4.82e+01
44	90	3.0	1481	19	M03740 rh528 gene product	4.82e+01
45	88	3.0	2351	3	P50319 Human antihemophilic	6.67e+01

ALIGNMENTS

RESULT 1
ID M37461 standard; Protein; 397 AA.
AC M37461; (first entry)
DE 21-MAY-1998
DT Mouse Ret ligand RetL3.
KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neuron disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Mus musculus.
PN M09744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
DR WPI: 98-018431/02.
DR N-PSDB: W00249.
PT New nucleic acid encoding ret receptor ligands and related prot-
PT - vectors, transformed cells and antibodies, used for promot-
PT growth and improving survival of injured cells, especially renal
PT nerve cells
PS Claim 2: Page 77-78; 113pp: English.
CC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,
CC deduced from cDNA clones (see W00249) isolated from an EST
CC database and by 5'RACE. Rat and human RetL1, human RetL2 and RetL3
CC sequences (see W37457-60 and W37462-63) are also claimed. RetL3
CC is a key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
CC cells transformed or transfected with these vectors are claimed, as
CC well as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to

CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SO Sequence 397 AA;

Query Match 93.9%; Score 2781; DB 28; Length 397;
 Best Local Similarity 92.9%; Pred. No. 4,986-267;
 Matches 369; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

Db 1 mglsprpplmlllvislwpjlgsgnsatenrfvnsctgarkkceanpackaayqh 60
 Oy 1 MGLSRSPRPPLVILLVLSTLMLPLGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQH 60
 Db 1 gactslsrplpdeesamaadcleaeedjrnslldrcbrrmkhbatcdlywvthpa 120
 Oy 1 LDSCTFPLSPFLSGESATSAACLEAAQOLRNSSLIDCRHRRRKHOATCLDIYTVHPV 120
 Db 121 tsjgdyeladvpyedvtstskpwmkmlsklmkpsdclclfamclclndkcdrlrkayg 180
 Oy 121 RSLGDEYLDVSPYEDVTSTSKPWMKMNLSKLSMKRPDSOLCLFAMLCCLNDKCDRLRAAYG 180
 Db 181 eacsgitcgrhclagrlstfexkaeshaaglllpcapedagcgerrrtlapscals 240
 Oy 181 EACSGICGRHCLAGRLSTFEXKAESHAAGLLCLPCAPEDAGCGERRRNTIAPSCALPS 240
 Db 241 vtpncdlrscfrcadpircrlnmldfchbpmldlfgcacegscrlaylgilgtamtgn 300
 Oy 241 VAPNCDLRSCFRADPIRCRLNMDFOHCHPMDLGTCATGOSRCLAYLGLGTAMTPN 300
 Db 301 flskvntvalgctrcsgnldqceceqlersfsqnpclvealaakmfhrqlfsqdwads 360
 Oy 301 FISVNTVALGCTRCSGNLDQCECEQLERSFSQNPCLVEALAAKMFHRQLFSQDWADS 360
 Db 361 tfsvvqgqnsnpalrlqrlpirlisfslp11lllqclw 397
 Oy 361 TFSVMOQNSPALRPLRLPVLVSFFLTLILQLTW 397

RESULT 2

ID W37463 standard; Protein: 400 AA.

AC W37463;
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL3.
 KW Ret ligand; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN WO9744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nedel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00251.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 - vectors, transformed cells and antibodies, used for promoting cell

PT growth and improving survival of injured cells, especially renal or
 PT nerve cells.

PS Claim 2; Page 85-86; 113pp; English.
 CC This amino acid sequence comprises human Ret ligand (RetL3,
 CC deduced from cDNA clones (see V00251) isolated from a adult heart
 CC and spinal cord libraries. Rat and human RetL3, human RetL2 and
 CC mouse RetL3 sequences (see W37457-62) are also claimed. Human
 CC RetL3 is 34.3% identical to human RetL1, 34.9% identical to human
 CC RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key
 CC component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing retL3 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL3. Its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SO Sequence 400 AA;

Query Match 79.9%; Score 2366; DB 28; Length 400;
 Best Local Similarity 77.5%; Pred. No. 1,426-224;
 Matches 306; Conservative 52; Mismatches 34; Indels 3; Gaps 3;

Db 6 nprlpjrvvllmlllpsppldaagdp1p1esrlmsnclgarkcgadp1csaaayhld 65
 Oy 6 nprlpjrvvllmlllpsppldaagdp1p1esrlmsnclgarkcgadp1csaaayhld 65
 Db 6 srrp-pplvi-ltlvslw-lplgtgns1ptenrlvnsctqarkkceanpackaayohld 62
 Oy 6 srrp-pplvi-ltlvslw-lplgtgns1ptenrlvnsctqarkkceanpackaayohld 62
 Db 66 scstslstlpseepvpddcleaaqqlnslslgcmchrrmkhbatcdlywvthraas 125
 Oy 66 scstslstlpseepvpddcleaaqqlnslslgcmchrrmkhbatcdlywvthraas 125
 Db 63 scfp1sslp1p1sgesatsaacleaaqolrnsslidcrhrrrkhoatcdlywvthpvn 122
 Oy 63 scfp1sslp1p1sgesatsaacleaaqolrnsslidcrhrrrkhoatcdlywvthpvn 122
 Db 126 lgnveladvpyedvtstskpwmkmlsklmkpsdclclfamclclndkcdrlrkayg 360
 Oy 126 lgnveladvpyedvtstskpwmkmlsklmkpsdclclfamclclndkcdrlrkayg 360
 Db 123 lgedyeldvspyedvtstskpwmkmlsklmkpsdclclfamclclndkcdrlrkayg 362
 Oy 123 lgedyeldvspyedvtstskpwmkmlsklmkpsdclclfamclclndkcdrlrkayg 362
 Db 186 cspghcgrhclagrlstfexkaeshaaglllpcapedagcgerrrtlapscals 362
 Oy 186 cspghcgrhclagrlstfexkaeshaaglllpcapedagcgerrrtlapscals 362
 Db 183 csgircgrhclagrlstfexkaeshaaglllpcapedagcgerrrtlapscals 362
 Oy 183 csgircgrhclagrlstfexkaeshaaglllpcapedagcgerrrtlapscals 362
 Db 246 pncldlrscfrcadpircrlnmldfchbpmldlfgcacegscrlaylgilgtamtgn 302
 Oy 246 pncldlrscfrcadpircrlnmldfchbpmldlfgcacegscrlaylgilgtamtgn 302
 Db 306 svntsvaalscscrgsnldqceceqlersfsqnpclvealaakmfhrqlfsqdwads 362
 Oy 306 svntsvaalscscrgsnldqceceqlersfsqnpclvealaakmfhrqlfsqdwads 362
 Db 303 skvntvalgctrcsgnldqceceqlersfsqnpclvealaakmfhrqlfsqdwads 362
 Oy 303 skvntvalgctrcsgnldqceceqlersfsqnpclvealaakmfhrqlfsqdwads 362
 Db 366 avmahqnpavrpqwpvslfscclp11lllslw 400
 Oy 366 svmoqnsPALRPLRLPVLVSFFLTLILQLTW 397

RESULT 3

ID W37465 standard; Protein: 346 AA.

AC W37465;
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand RetL3 partial sequence.
 KW Ret ligand; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;

Query	Match	Best Local Similarity	Score	DB	Length
Matches 310; Conservative 10; Mismatches 10; Indels 0; Gaps 0;	79.2%;	93.9%;	2347;	28;	346;
Sequence 346 AA;					
DR N-PSDS: V00235.					
PT New nucleic acid encoding ret receptor ligands and related proteins					
PT - vectors, transformed cells and antibodies, used for promoting cell					
PT growth and improving survival of injured cells, especially renal or					
PT nerve cells					
PS Disclosure: Page 73-74, 113pp: English.					
CC This polypeptide comprises a partial sequence of mouse Ret ligand					
CC RetL3, deduced from ESR A4050083 cDNA (see V00255). A full-length					
CC mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse					
CC and human RetL1, RetL2 and RetL3 cDNA sequences (see V00245-51) and					
CC encoded polypeptides (see W37457-63) are claimed and can be used					
CC in methods for promoting cell growth and improving survival of					
CC cells, especially renal or neural cells.					
DB 17 LSPDLPleesamsadcleaaeqrlnsjldcrchrnmkqatcldlywtvnparslgye 76					
OY 68 LSPPLPSESMATSAACLEAAQGLNSSLIDRCRHRKKNHQTCLDIWTYVNPVNSLDYE 127					
DB 77 Ldvsygedvtskwpkmnlsklmnlkpdsdclclxfamclthdkcdtllrkaygeacsgir 136					
OY 128 LDVSPYEDTIVTSKPKMKNLSTLSMLKLPDSDCLTFAMCLTLDNCDRLRKAYGACSGIR 187					
DB 137 cqrhlciaqlsrfekaeeshagqlllcpcepdaagcgerrrnrlapascapstppncld 196					
OY 188 CORHCLTALQKLSFFEKAEASHAGQGLLCPCAPEDAGCGERRRNTIAPSCALPVAAPCLD 247					
DB 197 lrfcfeadpplrslmfdqthchpmdllygcatcagrcrlaylglgtamrpnfiskvnt 256					
OY 248 LRSTCRADPLCRSLMDQTHCHPMDLIGTATGTSQRLRAYLGLGTAMRPNFISKVNT 307					
DB 257 tvaistcrtsgnslqdeecqrlersfgnqplvealaakmrfrhrgllfsqdwadstfsvvq 316					
OY 308 TVALGCTCRSGNQLQDECEQLEKSPSQPCLMELIAAKMFRHRLFGSDVADSTFSVWQ 367					
DB 317 qnsnpalrlqprlplslfslpllllglc 346					
OY 368 QNSSPALRPQRLPLVLSFFILTLILQTLW 397					
RESULT 4					
ID W37462 standard; Protein: 315 AA.					
AC W37462;					
DE 21-MAY-1998 (first entry)					
Human Ret ligand RetL3 partial sequence.					
KW Ret ligand: RetL; RetL3: receptor; signal transduction; human;					
KW cell growth; renal cell; nerve cell; renal failure; nephritis;					
KW kidney transplant; toxic injury; hypoxic injury;					
KW neurodegeneration; motor neuron disease; multiple sclerosis;					
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;					
KW cranial nerve injury; spinal cord injury; Down's syndrome;					
KW cerebral palsy; Lyme disease; muscular dystrophy;					
KW myasthenia gravis; tumour; therapy.					
OS Homo sapiens.					
PN W09744356-A2.					

[illegible]

AC W37460: (first entry)
 DT 21-MAY-1998
 DE Human Ret ligand RetL2.
 KW Ret ligand; RetL2; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN M09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; 007726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOI) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 N-PSDB: V00248.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 69-70: 113pp: English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL2,
 CC deduced from a cDNA clone (see V00248) isolated from a human foetal
 CC liver library. Rat and human RetL, and human and mouse RetL3
 CC sequences (see W37457-59 and W37461-63) are also claimed. Human
 CC RetL2 is 49.1% identical to human RetL protein. RetL is a
 CC key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL2 DNA and prokaryotic or eukaryotic host
 CC cells transfected or transfected with these vectors are claimed, as
 CC well as a method for production of RetL2, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL2, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SO Sequence 464 AA.

Query Match 25.6% Score 759; DB 28; Length 464;
 Best Local Similarity 37.3%; Pred. No. 9, 15e-62;
 Matches 120; Conservative 78; Mismatches 99; Indels 25; Gaps 18;

Db 40 cyranelcaeaencsrytlr-qc---lagr-drintmlnkcegaalevgspjydcrc 95
 Oy 41 CTQARRKCCANPCKAAAOHLDSCRPSLPSEGSATSAACLEMAOOLRRSSSLDCC 100
 Db 96 krgmkkelqclqywslnlgltege-efyeasrypevntadifrlaifsgadpvy 154
 Oy 101 HRRMNGAATCLDIWTVNHRVRLGDEL-DVSPYEDTV--SKPKM-NL-S-K-L-SKL 152
 Db 155 sakshcdaaekacnldnckllrissyisicmreispertcnrrckhalkrfidrvpse 214
 Oy 153 KPDSDCLKFAMLCTLINDCRRLKRAYGACS-GI----RCGRHCLMGALRSFFEKAES 207
 Db 215 ylyrnlfesc-qdga-caerrtqltlpscsyedkekncldlrycrtchlsrfaadh 272
 Oy 208 HAQGLLPCAPEDAGCGERRRRTIAPSCALPSVA-PNCLDRSFCRADPLCRSLMDFQ 266

Db 273 ancrasygtvscpadnhyacaglsyagmifgdnptnydsptglvypwscrcsganne 332
 Oy 267 TRHHPM-DILGTCATQSR-CLRAYGLTGTATPWFISKVITVALG--CTCRSGNLQ 322
 Db 333 eeceklrldfctenpclna1q 354
 Oy 323 DECEQLEKSFQNPCLMEATIAA 344

RESULT 6
 ID W37459 standard; Protein; 460 AA.
 AC W37459;
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL.
 KW Ret ligand; RetL; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN M09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; 007726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOI) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 N-PSDB: V00247.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 64-66: 113pp: English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL1,
 CC deduced from a cDNA clones (see V00247) isolated from a human
 CC foetal kidney. Rat RetL1 and mouse and human RetL2 and RetL3
 CC sequences (see W37457 and W37460-63) are also claimed. The
 CC human RetL1 sequence is 93.3% identical to that of rat. Ret ligand
 CC is a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor, triggering Ret dimerisation and/or
 CC autophosphorylation of the Ret tyrosine kinase domain. Vectors
 CC containing RetL1 DNA and prokaryotic or eukaryotic host cells
 CC transfected or transfected with these vectors are claimed, as well
 CC as a method for production of RetL1, its soluble variants and fusion
 CC proteins with a toxin, imageable compound or radionuclide. RetL1,
 CC optionally when expressed from vectors in vivo, is used to promote
 CC growth of new tissue and survival of damaged tissue, particularly
 CC kidney or neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SO Sequence 460 AA.

Query Match 25.1% Score 744; DB 28; Length 460;
 Best Local Similarity 37.0%; Pred. No. 2, 83e-60;
 Matches 128; Conservative 70; Mismatches 126; Indels 22; Gaps 19;

Db 3 latyfalpl-ldlllaesvggdr1-d-cvksadqclkeascaktytlrgevagketn 59
 Oy 12 LVILLVLVSLWLPGTGNSLPTENRLVNSCTQARKKEANPACAAAOHLDSCRPSL-SS 70


```

Db      241  VAPNCLDLSPFRADPLCRSLRMLDMQYCHPMIDIGTCATQSSCLRAYIGLIGTATPN 300
      241  VAPNCLDLSPFRADPLCRSLRMLDMQYCHPMIDIGTCATQSSCLRAYIGLIGTATPN 300
Oy      301  FTSKVVTTVALSCTCRGSGNLQDECEQELERSFSQNPCLVEAIAKMFHRLQFSQWADS 360
      301  FTSKVVTTVALSCTCRGSGNLQDECEQELERSFSQNPCLVEAIAKMFHRLQFSQWADS 360
Oy      301  FTSKVVTTVALSCTCRGSGNLQDECEQELERSFSQNPCLVEAIAKMFHRLQFSQWADS 360
      301  FTSKVVTTVALSCTCRGSGNLQDECEQELERSFSQNPCLVEAIAKMFHRLQFSQWADS 360
Db      361  TFSVVOQOONSAPALRLQRLPLPSILPLILQTLW 397
      361  TFSVVOQOONSAPALRLQRLPLPSILPLILQTLW 397
Oy      361  TFSVVOQOONSAPALRLQRLPLPSILPLILQTLW 397
      361  TFSVVOQOONSAPALRLQRLPLPSILPLILQTLW 397

RESULT      2
ENTRY
TITLE      gas1 homolog - human
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94173926
#status
#molecule_type mRNA
#residues
#cross-references GB:LI3696; NID:9472859; PID:9472860
#length 345 #molecular_weight 35721 #checksum 570
SUMMARY

Query Match      3.9%; Score 115; DB 2; Length 345;
Best Local Similarity 31.9%; Pred. No. 2,31e-03;
Matches 22; Conservative 19; Mismatches 24; Indels 4; Gaps 3;

Db      24  LMAILQLGSAAPRSGLAHGRRLI-CWQALLQCGEPESYAYNOYAECAPVLAQH-G 80
      24  LMAILQLGSAAPRSGLAHGRRLI-CWQALLQCGEPESYAYNOYAECAPVLAQH-G 80
Oy      15  LLLVLSLWLPGLTGNSLPTENRLVNSTOARKCEANPACKAAV-QHLDSCPTSLSSPLP 73
      15  LLLVLSLWLPGLTGNSLPTENRLVNSTOARKCEANPACKAAV-QHLDSCPTSLSSPLP 73
Db      81  GGDAPGAA 89
      81  GGDAPGAA 89
Oy      74  GGSATSHA 82
      74  GGSATSHA 82

RESULT      3
ENTRY
TITLE      gas1 protein - mouse
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:92370681
#accession
#status
#molecule_type mRNA
#residues
#cross-references EMBL:X65128; NID:951045; PID:951046
GENETICS
KEYWORDS
SUMMARY

Query Match      3.9%; Score 115; DB 2; Length 384;
Best Local Similarity 33.9%; Pred. No. 2,31e-03;
Matches 21; Conservative 16; Mismatches 22; Indels 3; Gaps 2;

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Db      58 PALLCUALAOLQCSARSGGLAHGRLLI--CQNALOCGSGDDPSVAASOYAENACAP 115
QY      9 PEPYVILLVLSLMPLETGNSLPTERNLVNCTQARKKCEAMPACKAAI-OHLDSCTPS 67
Db      116 LA 117
QY      68 LS 69

RESULT 4
ENTRY   #type complete
TITLE   adaptive response regulatory protein - Escherichia coli
CONTAINS
ORGANISM
DATE    #format_name Escherichia coli
        28-Dec-1987 #sequence_revision 05-Dec-1997 #text_change
        05-Dec-1997
ACCESSIONS
REFERENCE
#authors
Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao
Y.
#journal
#title      Science (1997) 277:1453-1462.
#cross-references MUID:97426617
#accession  C64991
#status
#molecule_type DNA
#residues   1-354 #label BLAT
#cross-references GB:AE000310; GB:U00096; NID:g2367131; PID:g1788542;
        IMG_P:02213
REFERENCE
#experimental_source strain K-12, substrain MG1655
A22630
#authors
Nakabeppu, Y.; Kondo, H.; Kawabata, S.; Iwanaga, S.;
Sekiyauchi, M.
#journal
#title      J. Biol. Chem. (1985) 260:7281-7288
        Purification and structure of the intact Ada regulatory
        protein of Escherichia coli K12, O(6)-methylguanine-DNA
        methyltransferase.
#cross-references MUID:85207761
#accession  A22630
#molecule_type DNA
#residues   1-133,'R',135-354 #label NAK
#cross-references GB:M10211; NID:g145188; PID:g145189
#experimental_source strain K12
REFERENCE
#authors
Dempfle, B.; Sedgwick, B.; Robins, P.; Totley, N.; Waterfield,
M.D.; Lindahl, T.
#journal
#title      Proc. Natl. Acad. Sci. U.S.A. (1985) 82:2688-2692
        Active site and complete sequence of the suicidal
        methyltransferase that counters alkylation mutagenesis.
#cross-references MUID:85190562
#accession  A22667
#molecule_type DNA
#residues   1-774,'D',76-78,'PR',81-317,'V',319-329,'S',331-354
        #label DEM
#cross-references GB:M10315; NID:g145190; PID:g145191
#experimental_source strain B/r
REFERENCE
#authors
Nakabeppu, Y.; Sekiyauchi, M.
#journal
#title      Proc. Natl. Acad. Sci. U.S.A. (1986) 83:6297-6301
        Regulatory mechanisms for induction of synthesis of
        enzymes in response to alkylating agents: Ada protein
        as a transcriptional regulator.
#cross-references MUID:86313568
#accession  I41114
#status
#molecule_type DNA
#residues   1-27 #label RES
#cross-references GB:M13828; NID:g145196; PID:g145197

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OY 121 RSLGDELDVSPYEDVTYSKPMKMLSKLMLKPSDCLKFAMLCTLNDKCDRLKAYG 180
DB 181 EACSGIRCORHICLAQLRSFEFEKAESHAQGLLCPACAPEDAGCGERRNTIAPSCALPS 240
OY 181 EACSGIRCORHICLAQLRSFEFEKAESHAQGLLCPACAPEDAGCGERRNTIAPSCALPS 240
DB 241 VTPNCLDLRSFCRADPLCRSLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
OY 241 VTPNCLDLRSFCRADPLCRSLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
DB 301 FISKVNTTVALSCTCRSGSNLQDECEOLERSFSQNPCLVEATIAAKMFRHROLFSQDMADS 360
OY 301 FISKVNTTVALSCTCRSGSNLQDECEOLERSFSQNPCLVEATIAAKMFRHROLFSQDMADS 360
DB 361 TFSVVOOONSPPALRPLQPLILSFILPILILQTLW 397
OY 361 TFSVVOOONSPPALRPLQPLILSFILPILILQTLW 397

RESULT 2
ID 035325 PRELIMINARY: PRT: 397 AA.
AC 035325:
BT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFRA-3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROSNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA TRUMP M., RAYNOSCHER C., IBANEZ C.F.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF020305; G2429367; -.
SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

Query Match 93.8%; Score 2778; DB 11; Length 397;
Best Local Similarity 92.7%; Pred. No. 0.00e+00;
Matches 368; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

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DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFRA3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROSNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENFALK J., TOMAC A., LINDOVIST E., HOFFER B., OLSON L.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA MAYEILHAN P., BAUDER C., MIKAELS O., SHEN L., WESTPHAL H., ERNFORS P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1997).
DR EMBL: AF041842; G2921579; -.
DR EMBL: AF036163; G2674177; -.
SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 93.4%; Score 2766; DB 11; Length 397;
Best Local Similarity 92.4%; Pred. No. 0.00e+00;
Matches 367; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

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RL  PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
RP  [2]
RC  SEQUENCE FROM N.A.
RA  SANICOLA M., HESSION C.A., WORLEY D.S., CARNILLO P., EHRENFELS C.,
RA  WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA  PENINSKY R.B., CATE R.L.;
RL  SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  TISSUE-SUBSTANTIA NIGRA;
RA  HISHIKI T., KONDOH K., ICHIMIYA S., NIMURA Y., SEKI N., OZAKI T.,
RA  SAKIYAMA S., TAKAHASHI H., OHNUMA N., TANABE M., FUJIMURA S.,
RA  NAKAGAWARA A.;
RL  SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR  EMBL: U97144; G2282026; -
DR  EMBL: U95847; G2459742; -
SQ  SEQUENCE 460 AA; 50838 MW; 022FECA CRC32;

Query Match          25.1% Score 744; DB 4; Length 460;
Best Local Similarity 37.0% Pred. No. 9,606-155;
Matches 128; Conservative 70; Mismatches 126; Indels 22; Gaps 19;

Db  3 LATIVEPALP-LDILLLSAEVSGDRL-D-CYKASDOCLEKSCSTKYRTLRCQVAGKETN 59
Qy  12 LVILLVLSTLWPLGTGSLPTENLVNSCTQARKKCCANACAAVOHLDSCPSL-SS 70
Db  60 FLSASGLEAKE-CRSAEALAKOKSLVYCRCKRCKGKKKCKRLRIYMSY--QSLQGNDL 116
Qy  71 -PLPGEBSATPAACLEAAQQLRNSSLIDCRHRKRRKQATCLDIYVTHPVRSIGDEL- 128
Db  117 EDSPSE-PVNSRLSDIFEVVPISEVHPIKKNCLIDAKACNPDICKKYRSAYITPCTT 175
Qy  129 DVSPEDEVTSKPKKM-NLSK-LSMK-PSDCLCFKAMLCITLNDKCDRLKATGEACS- 184
Db  176 SVSNDVCRKRRCHALRFQEDKVPAAKSHYGMIFCSC-R-DIACERRRQTIIVPCSYEER 233
Qy  185 GIR--CORHLCQLQLTSFFEKAAESHAQGLLCPCAPEDAGCGERNRNTIAPSCALPSV 241
Db  234 EKPCNLNODSCKKNYICRSLADFTFNCPESPESVSSCLKENYADCLLAYSGLIGTVM 293
Qy  242 A-PMCLDRSCGRADPLCRSLMDFOHCHPMDI-LGTCACTE-SRLCRLAYGLIGTAMT 298
Db  294 PNYIDSSLYAPWCDCSNSGNDLEECLEKLFNFKNDTCKKNIAQA 339
Qy  299 PNFISKVNTVVALGCTCRGSGNQDDEQLEKSSQNPCIMEAIIA 344

RESULT          9
ID  035252      PRELIMINARY;          PRT;          463 AA.
AC  035252;
DT  01-JAN-1998 (TREMBLREL. 05, CREATED)
DT  01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DI  01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE  GNF RECEPTOR BETA.
GN  GNF-R-BETA.
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
CC  SUGIUGNATHI; MURIDAE; MURINAE; MUS.
LN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-C57;
RA  DEY B.K., WONG Y.W., TOO H.P.;
RL  NEUROREPORT 9:0-0(0001).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-C57;
RA  DEY B.K., WONG Y.W., TOO H.P.;
RL  SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR  EMBL: AF015172; G2624963; -
SQ  SEQUENCE 463 AA; 51134 MW; 910E17F CRC32;

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 W27327
 (TM)

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:49:21 1999; Maspar time 16.79 Seconds

Tabular output not generated. 480,061 Million cell updates/sec

Title: >US-08-866-354-43
 Description: (1-498) from US08866354.pep
 Perfect Score: 2337
 Sequence: 1 MVXXLXXXPXPXXMXLX.....XLPVLMTLALXLSXXXXS 498

Scoring table: PAM 150
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29

Statistics: Mean 32.365; Variance 142.853; scale 0.227

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1803	77.2	468	27	W27327	Rat glial cell derive
2	1803	77.2	468	28	W35334	Rat glial cell line-d
3	1803	77.2	468	28	W37457	Rat Ret ligand RetL1
4	1788	76.3	464	28	W37460	Human Ret ligand RetL
5	1783	76.3	465	28	W35333	Human Ret ligand RetL
6	1732	74.1	460	28	W37458	Human Ret ligand RetL
7	1703	55.8	346	28	W37458	Human Ret ligand RetL
8	1030	44.1	400	28	W37461	Human Ret ligand RetL
9	982	43.0	397	28	W37461	Human Ret ligand RetL
10	866	37.1	346	28	W37465	Mouse Ret ligand RetL
11	826	35.3	315	28	W37462	Mouse Ret ligand RetL
12	96	4.1	1251	14	R79475	Human Ret ligand RetL
13	93	4.0	469	20	W03448	Farnesoid-activated r
14	93	4.0	1480	5	R25079	Drosophila slit prote
15	92	3.9	383	10	R56166	Neuroendocrine tumor
16	92	3.9	833	6	R28960	Delta D11
17	91	3.9	2189	1	R05222	Antigen GMS401FL enco
18	88	3.8	385	10	R56167	Neuroendocrine tumor

Result ID	Score	Query Match	Length	ID	Description	Pred. No.
19	89	3.8	509	8	R41920	MISR1
20	89	3.8	509	13	R70239	Serine/threonine kin
21	88	3.8	509	18	W03759	Mullerian inhibiting
22	88	3.8	686	28	W25719	Human alpha meltrin p
23	89	3.8	1712	4	R22461	Masking protein high
24	89	3.8	1810	16	R94563	Chicken cytotactin
25	87	3.7	559	1	P94403	Analogue of amino aci
26	87	3.7	816	27	W37501	Human nel-related pro
27	87	3.7	903	28	W25715	Mouse alpha meltrin p
28	83	3.6	182	3	R10872	Protein encoded by me
29	83	3.6	207	28	W25720	Human alpha meltrin p
30	85	3.6	223	23	W21733	NIP-1 encoded by clon
31	83	3.6	328	20	R89272	Insulin like growth f
32	83	3.6	328	1	R04908	ECORI-ECORI fragment
33	84	3.6	618	6	R29928	Elmeris antigen Eam10
34	83	3.6	630	14	R76074	Human 5HT transporter
35	83	3.6	630	7	R34664	Human 5HT transporter
36	85	3.6	947	28	W42402	Amino acid sequence o
37	84	3.5	3164	16	R94346	Hepatitis GB virus (H
38	82	3.5	226	3	R13757	Proactin
39	81	3.5	559	17	R86223	Novel plasminogen act
40	81	3.5	559	17	R86222	Novel plasminogen act
41	81	3.5	578	28	W33398	Human haematopoietic
42	81	3.5	636	28	W33399	Alternatively spliced
43	81	3.5	1055	29	W44298	Human serrate 2
44	81	3.5	1212	29	W44299	Human serrate 2
45	81	3.5	1257	20	W05834	Human Serrate-2 (H2)

ALIGNMENTS

RESULT 1
 ID W27327 standard; protein; 468 AA.
 AC W27327; 1998 (first entry)
 DT 27-APR-1998
 DE Rat glial cell derived neurotrophic factor receptor alpha.
 KW GDNF; rat; Kidney disease; glomerulonephritis; therapy.
 OS Rattus sp.
 FT Key
 FT Peptide
 FT Location/Qualifiers
 FT 1..24
 FT /label= sig_peptide
 FT 25..445
 FT /note= "extracellular domain"
 FT Domain
 FT 446..468
 FT /note= "GPI-attachment site"
 FT Modified_site
 FT 61
 FT /note= "O-glycosylated"
 FT Modified_site
 FT 349
 FT /note= "O-glycosylated"
 FT Modified_site
 FT 408
 FT /note= "O-glycosylated"
 FT Cleavage_site
 FT 428..430
 FT /note= "GPI-anchor cleavage/attachment site"
 FT W09733912-A2.
 PD 18-SEP-1997
 PR 13-MAR-1997; U04363.
 PR 14-MAR-1996; US-618236.
 PR 14-MAR-1996; US-615902.
 PA (GERTH) GENENTECH INC.
 PI Klein RD, Moore MW, Rosenthal A, Ryan AW;
 DR WPI: 97-470819/43.
 DR N-PSDS: T84975.
 PT Isolated glial cell derived neurotrophic factor receptor alpha
 PT useful to develop products to diagnose and treat associated
 PT disorders, particularly enteric nervous system or kidney disorders
 PS Claim 1; Page 78-79; 100pp; English.
 CC This protein comprises full-length rat glial cell derived
 CC neurotrophic factor receptor alpha (GDNFR alpha), a novel
 CC GPI-linked protein that is a ligand-binding component of the
 CC receptor system for GDNF. Its amino acid sequence was deduced
 CC from an isolated cDNA clone (see T84975). The invention relates
 CC to novel uses of GDNF and its receptor. In particular, it

CC relates to native rat GDNF alpha (see W27327), its variants and
 CC soluble derivatives (extracellular domain), chimeric GDNF alpha
 CC and antibodies which bind to the GDNF alpha, including agonist
 CC and neutralising antibodies, as well as various uses for these
 CC molecules. It also relates to assay systems for detecting ligands
 CC to GDNF alpha, systems for studying the physiological role of
 CC GDNF, diagnostic techniques for identifying GDNF-related conditions,
 CC methods for identifying molecules homologous to GDNF alpha, and
 CC therapeutic techniques (claimed) for the treatment of GDNF-related
 CC and GDNF alpha-related conditions, particularly kidney disease
 CC associated with glomerulonephritis and enteric nervous system
 CC related disorders. Transgenic and knockout animals are also
 CC claimed.
 SQ Sequence 468 AA:

Query Match 77.2% Score 1803; DB 27; Length 468;
 Best Local Similarity 53.3%; Pred. No. 1,336-159;
 Matches 255; Conservative 23; Mismatches 183; Indels 17; Gaps 12;

b 1 mfiatlyfalplldlmsaevsagdr1--dcvkaadqclkegscstkyrtlrqvagket 58
 16 MVLXLLSLALPLXKXQGEELKXKXLDVCVAXXKCAEXXCSXXRTLROCAAGXXX 75
 Db 59 nfiatlglaekde--crsamealkqkslyncrcrkqgmkeknclrlwsmysq1g-gnd1 115
 76 NTYXLASGXEXXKXKXKXEXLXSSLYDCRCRKGMRKEXXCLXIYWSHXHXXLXGNXX 135
 Db 116 ledsprep-vnsrladifravflsdvfgvhehlskgnncldaaekcnldtckkyrsay 174
 136 LEXSPREPXYVTSRLSDIRFXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 195
 Db 175 ltpcttsman-evcnrrkchkalkrfidkvpakhsygmalfcscr--diacterrrtglvp 231
 196 IXXCXXXKXEXERCNRKCHKALROFDPKVPXHXHGMFCSCXXDXDAKCHERRQTIYP 255
 Db 232 vcsyeerpcncls1qdscktnylcrsrladifncqpesrsvsnclkenyadcllayag 291
 256 SCSYEXXKXEPNCLDLRXKCRDTDLXCRSLADFTYCNKXKXKXKXKXKXKXKXKX 315
 Db 292 l1gvtmtpnyvds-sls-vapwcdsngndledclflnfkdntclkaalgaifngs 349
 316 L1GTMTPNYVDSSTYKXKXVAPWCRCRSGKXKXKXKXKXKXKXKXKXKXKXKXKX 375
 Db 350 dvtmwqpa--p--pvqtatcttafrvknkp-1gpasene-1pbnvlppcanlgaqk1 403
 376 XXXXXXXXXKXFXVXXXXXXXTXKXKXVXKXSLKXKXKXKXKXKXKXKXKXKXKX 435
 Db 404 knvsgschlclsdadfgkdlagasshlctksmaappscals1pvlmltalaa1ls 461
 436 KKNXSXEXXKXCFXELTXXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 493

RESULT 2
 ID W35334 standard; Protein: 468 AA.

AC W35334;
 DT 01-MAY-1998 (first entry)
 DE Rat glial cell line-derived neurotrophic factor receptor.
 KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.
 OS Rattus sp.
 PN M09740157-A1.
 PD 30-OCT-1997.
 PF 15-APR-1997; U06281.
 PR 14-APR-1997; US-837199.
 PR 22-APR-1996; US-015907.
 PR 09-MAY-1996; US-017221.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI: 97-535836/49.
 DR N-PSDB: T95297.

PT glial cell line derived neurotrophic factor receptor - useful to
 PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and
 PT Alzheimer's disease
 PS Claim 1: Pages 96-98; 196pp; English.
 CC The present sequence is the rat glial cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or amyotrophic lateral sclerosis, complications of diabetes
 CC and Huntington's disease and (optionally in combination with GDNF)
 CC glaucoma, retinal degeneration and hearing loss caused by injury to
 CC inner ear sensory neurons. The receptor can also be used to block
 CC unwanted GDNF activity, analyse GDNF related molecules and
 CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
 CC cells, preferably transfected ex vivo, can be used similarly by
 CC implantation, and the use of the receptor cDNA in gene therapy is
 CC also contemplated. Probes based on the cDNA can be used to identify
 CC GDNF responsive cells and tissues, e.g. to identify patients who
 CC would benefit from GDNF therapy, and abnormalities in receptor
 CC expression, and to isolate molecules that form a complex with the
 CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
 CC antibodies, oligonucleotides derived from the cDNA and animal
 CC models that overexpress the receptor can be used to study the
 CC biological function of GDNF, knockout transgenic animals can be
 CC used to detect GDNF dependent neurons or processes and the antibody
 CC can be used in immunoassays for the receptor. The receptor binds
 CC GDNF specifically and with high affinity, acting as part of a
 CC complex that mediates/enhances signal transduction by GDNF, i.e.
 CC increasing dopamine uptake in dopaminergic cells.
 SQ Sequence 468 AA:

Query Match 77.2% Score 1803; DB 28; Length 468;
 Best Local Similarity 53.3%; Pred. No. 1,336-159;
 Matches 255; Conservative 23; Mismatches 183; Indels 17; Gaps 12;

Db 1 mfiatlyfalplldlmsaevsagdr1--dcvkaadqclkegscstkyrtlrqvagket 58
 16 MVLXLLSLALPLXKXQGEELKXKXLDVCVAXXKCAEXXCSXXRTLROCAAGXXX 75
 Db 59 nfiatlglaekde--crsamealkqkslyncrcrkqgmkeknclrlwsmysq1g-gnd1 115
 76 NTYXLASGXEXXKXKXKXEXLXSSLYDCRCRKGMRKEXXCLXIYWSHXHXXLXGNXX 135
 Db 116 ledsprep-vnsrladifravflsdvfgvhehlskgnncldaaekcnldtckkyrsay 174
 136 LEXSPREPXYVTSRLSDIRFXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 195
 Db 175 ltpcttsman-evcnrrkchkalkrfidkvpakhsygmalfcscr--diacterrrtglvp 231
 196 IXXCXXXKXEXERCNRKCHKALROFDPKVPXHXHGMFCSCXXDXDAKCHERRQTIYP 255
 Db 232 vcsyeerpcncls1qdscktnylcrsrladifncqpesrsvsnclkenyadcllayag 291
 256 SCSYEXXKXEPNCLDLRXKCRDTDLXCRSLADFTYCNKXKXKXKXKXKXKXKXKX 315
 Db 292 l1gvtmtpnyvds-sls-vapwcdsngndledclflnfkdntclkaalgaifngs 349
 316 L1GTMTPNYVDSSTYKXKXVAPWCRCRSGKXKXKXKXKXKXKXKXKXKXKXKXKX 375
 Db 350 dvtmwqpa--p--pvqtatcttafrvknkp-1gpasene-1pbnvlppcanlgaqk1 403
 376 XXXXXXXXXKXFXVXXXXXXXTXKXKXVXKXSLKXKXKXKXKXKXKXKXKXKXKX 435
 Db 404 knvsgschlclsdadfgkdlagasshlctksmaappscals1pvlmltalaa1ls 461
 436 KKNXSXEXXKXCFXELTXXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 493

RESULT 3
 ID W37457 standard; Protein: 468 AA.
 AC W37457;
 DT 21-MAY-1998 (first entry)
 DE Rat Ret ligand RetL1.
 KW Ret ligand; RetL1; receptor; signal transduction; rat.

Accession	Location/Qualifiers	Label= Sig_peptide
OS Rattus sp.		
KW myasthenia gravis; tumour; therapy.		
KW cerebral palsy; Lyme disease; muscular dystrophy;		
KW cranial nerve injury; spinal cord injury; Down's syndrome;		
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;		
KW neurodegeneration; motor neurone disease; multiple sclerosis;		
KW kidney transplant; toxic injury; hypoxic injury;		
KW cell growth; renal cell; nerve cell; renal failure; nephritis;		
FT FT	1..24	
DR N-PSDB: V00245.		
DR MPI: 98-018431/02.		
PI cate RL, Hession C, Sanicola-Nadel M;		
PA (BIOJ) BIOGEN INC.		
PR 16-JUL-1996; US-021859.		
PR 07-JUN-1996; US-019300.		
PR 08-MAY-1996; US-017427.		
PR 10-APR-1997; US-01726.		
PD 27-NOV-1997.		
PN MO9744356-A2.		
FT FT		
CC This protein comprises rat Ret ligand (RetL), RetL, a key component		
CC of the Ret signalling pathway that specifically interacts with Ret		
CC receptor protein, triggering Ret dimerisation and/or		
CC autophosphorylation of the Ret tyrosine kinase domain.		
CC The amino acid sequence was deduced from a cDNA clone (see V00245) obtained		
CC from a rat embryonic kidney cDNA expression library. Human RetL		
CC as well as mouse and human RetL2 and RetL3 sequences have also been		
CC identified (see W37458-63). Vectors containing retL DNA and		
CC prokaryotic or eukaryotic host cells transformed or transfected		
CC with these vectors are claimed, as well as a method for production		
CC of RetL. Its soluble variants (e.g. amino acids 1-434) and fusion		
CC proteins with a toxin, imageable compound or radionuclide, RetL,		
CC optionally when expressed from vectors in vivo, is used to promote		
CC growth of new tissue and survival of damaged tissue, particularly		
CC kidney or neural tissue. Typical applications are in renal failure,		
CC nephritis, kidney transplants, toxic or hypoxic injury,		
CC neurodegeneration, motor neurone disease, multiple sclerosis,		
CC bacterial, viral or prion infections (e.g. meningitis, myelopathy		
CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or		
CC spinal cord injury, developmental disorders such as Down's syndrome		
CC and cerebral palsy, or conditions involving the peripheral nervous		
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).		
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing		
CC cells, especially tumours.		
CC Sequence 468 AA;		
SC		
Query Match 77.2%; Score 1803; DB 28; Length 466;		
Best Local Similarity 53.3%; Pred. No. 1.33e-159;		
Matches 255; Conservative 23; Mismatches 183; Indels 17; Gaps 12.		
Db 1 mflctlyfahplldalmsaevsqgdrl--devksdqclkgqsestyttrtlrgevsket 58		
Qy 16 MxLRLSLALPLAXXXLGGAEIXGXXRLXXDVCVAXXXXCXAXXCSXXRYRLRQXXAXXX 75		
Db 59 nfaitsglaeakde--craamealqkqsiynercrrgmkkkencrlrlywsmysiq-gndl 115		
Qy 76 NTXLASGEXEXXXXXXAXEXLXSSLSYDRCRCRGMKKEXXCLXITWSSHXIXLXGNXX 135		
Db 116 ledspyeep-vnsrlsdlfravpflsdvfqgvshskgnncldaaecnldctckkysay 174		
Qy 136 LEXSPYEXXVTSRISDIFRXSXSSXXSXDXXXXXXKSSXMCIDAKACNLNDXCKRLRSAY 195		
Db 175 ltpcttsmsn-evcnrrtckhkalvgfdkvpahskysgmflfsc--dlaccerrrrtlvp 231		
Qy 196 IXXCXXXXXXEKRRCRRRCHALRQFEVKVYXXKHVIGLTFSCXXXXXADACKERRRQITXP 255		

D
232 vcsyeerpcnclsgdckcnyrcrldfftnccpsarvscikenydcilaysg 29

QY 256 SCGYEKXKEKPNCLDRXXCRFDLKRRLADFTNCKXXXRRVXSCKXANXYXCCLAAVG 31

D
292 llyvtmtpnyvdss-sls-vapwcdcsangndedclktinfkntctlkmaigefngs 745

QY 316 LICTMYTTPRYVDSSXTXXXVAPMCKRGSGNNXXEECEKFLEFXFNPCLNMAIOAFGN:X 78

D
350 dvumwpa--p--pyqtatttatafrvhkp-lypgseane-iphvlyppcaulgqy 94

QY 376 XXXXXXXXXXXPEFYVXXXXXXXTAKRVXXXXPSLLXXXXXXLLTXVXXCXKXUXCN: 97

D
404 kenvgssthlclsdgdfgkdglagasshtlckmaepscslsljpvmltalaaals 103

QY 436 KMXKSXXXXXCKXELTTXXXXXXSGXXXXXXSXKXAXPVALXXLPVLMTLRALALS 403

RESULT 4

ID W37460 standard; Protein: 464 AA.

AC W37460:

DE 21-MAY-1998 (first entry)

Human Ret ligand RetL2.

KW Ret ligand; RetL; RetL2; receptor; signal transduction; human;

KW cell growth; renal cell; nerve cell; renal failure; nephritis;

KW kidney transplant; toxic injury; hypoxic injury;

KW neurodegeneration; motor neurone disease; multiple sclerosis;

KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;

KW cranial nerve injury; spinal cord injury; Down's syndrome;

KW cerebellar palsy; Lyme disease; muscular dystrophy;

KW myasthenia gravis; tumour; therapy.

OS Homo sapiens.

PN M097443356-A2.

PD 27-NOV-1997.

PF 07-MAY-1997; U07726.

PR 10-APR-1997; US-017427.

PR 08-MAY-1996; US-017427.

PR 07-JUN-1996; US-019300.

PR 16-JUL-1996; US-021859.

PA (BIOJ) BIOGEN INC.

PI Cate RL, Hession C, Santicola-Nadel M;

DR WPI; 98-018431/02.

DR N-PSDB: V00248.

PT New nucleic acid encoding ret receptor ligands and related proteins

PT - vectors, transformed cells and antibodies, used for promoting cell

PT growth and improving survival of injured cells, especially renal or

PT nerve cells

PS Claim 2: Page 69-70; 113pp: English.

PS This amino acid sequence comprises human Ret ligand (RetL) RetL2,

CC deduced from a cDNA clone (see V00248) isolated from a human foetal

CC liver library. Rat and human RetL1, and human and mouse RetL3

CC sequences (see W37457-59 and W37461-63) are also claimed. Human

CC RetL2 is 49.1% identical to human RetL protein. RetL is a

CC key component of the Ret signalling pathway that specifically

CC interacts with Ret receptor protein, triggering Ret dimerisation

CC and/or autophosphorylation of the Ret tyrosine kinase domain.

CC Vectors containing retL DNA and prokaryotic or eukaryotic host

CC cells transformed or transfected with these vectors are claimed, as

CC well as a method for production of RetL2, its soluble variants and

CC fusion proteins with a toxin, imageable compound or radionuclide.

CC RetL2, optionally when expressed from vectors In vivo, is used to

CC promote growth of new tissue and survival of damaged tissue,

CC particularly kidney or neural tissue. Typical applications are in

CC renal failure, nephritis, kidney transplants, toxic or hypoxic

CC injury, neurodegeneration, motor neurone disease, multiple sclerosis

CC bacterial, viral or prion infections (e.g. meningitis, myelopathy

CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or

CC spinal cord injury, developmental disorders such as Down's syndrome

CC and cerebral palsy, or conditions involving the peripheral nervous

CC system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC Fusion proteins are used to deliver toxins etc. to Ret-expressing

CC cells, especially tumours.

SQ Sequence 464 AA.

Query Match	76.5%;	Score 1788;	DB 28;	Length 464;
Best Local Similarity	56.2%;	Pred. No. 3,78e-158;		
Matches	26;	Conservative 17;	Mismatches 166;	Indels 21; Gaps 9

Db	19	slaaepsiaqgelbhw-pprvdcrrnlaeaaeancsrytllqclagrdtrnmlan-x	76
Qy	24	ALPLXXALQGELELGXKFLXDXCVYAAHXXCAEXKCSXHTYTLQCNAGXXHNTYLSGX	83
Db	77	e-----cqaalevlgaeaplydcrcctgmkkelqclqlywshlgltegeefyaaspuep	130
Qy	84	EXXXXXXXHXXEXELXHXSSLYDCKRCROMKEXXCLXHYGSHXXLXGXNXXLEXPYER	145
Db	131	-vtarledifflaasifsgtgedrprvvasahsnblaaakcnlnndckrlrissyisicmet	189
Qy	144	XVTSLSLSDIFHXXSKXXSXKXDXKXKXSNCKCLDPAKCNLNDCKRLRSYVIXXXCXXX	203
Db	190	sptecmrckhkaalrqfddrvpseytyrmlfscsq--dqacaertrqyllpsscyecke	247
Qy	204	SXXECCNRKCKHKLROGFDFKVPVPHXHXGMLFCSCXXHDXAKCBRRQTLIPSCSYEXHE	265
Db	248	kpnclldlgrvertdhlcrrsladfhancrasyqvtvscpadnyaqclisyagmfigfmdtr	307
Qy	264	KPNCLDLDEXXKCRTHYLCRSLADBYXTNCKXXHXXRVXXSCXANXXXXCLAXYVGLIGYKMP	322
Db	308	nyvasaprglvspwscsgrsgsmeececfldigttepcrlmaigafmgtdvtrvpkg	365
Qy	324	NYVSSXTHXXVAAWCMACRSGSGNXXEBCERLAFEXXNPFCLXNMLQAFGNCXXXXXXX	383
Db	368	--paf-----qa-tqapryektpslpddlsdstslgtsyvlctcstvyqegqlkanakel	418
Qy	384	XXPFYSVXXXXXXTHXAKRNVXXPSLXXXXXSLXLTYYXXCXHLOXOLKFXNXSEX	443
Db	419	smctfcltlnlpgsnkvlpknspsrtaipaaaltvsvlmklal	464
Qy	444	XXCFRLELTNNXXSGXHXHXXSXKXAPXALXHXPLVLLT-AL	488

RESULT 5 standard: Protein; 465 AA.
AC W35333;
DT 01-MAY-1998 (first entry)
DE Human glial cell line-derived neurotrophic factor receptor.
KW Human; glial cell line-derived neurotrophic factor; GDNF; receptor
KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
KW gene therapy.
MS Homo sapiens.
PN W09740152-A1.
PD 30-OCT-1997.
PE 15-APR-1997; U06281.
PR 14-APR-1997; US-837199.
PR 22-APR-1996; US-015807.
PR 09-MAY-1996; US-017221.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jjing S, Wen D;
DR MPI: 97-535836/49.
DR N-PSDB: T88419.
PT glial cell line derived neurotrophic factor receptor - useful to
PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and
PT Alzheimer's disease
PS Claim 1; Pages 91-93; 196pp; English.
CC The present sequence is the human glial cell line-derived
CC neurotrophic factor (GDNF) receptor, which can be used to treat
CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
CC disease or amyotrophic lateral sclerosis, complications of diabetes
CC and Huntington's disease and (optionally in combination with GDNF)
CC glaucoma, retinal degeneration and hearing loss caused by injury to
CC inner ear sensory neurons. The receptor can also be used to block
CC unwanted GDNF activity, analyse GDNF related molecules and
CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
CC cells, preferably transfected *ex vivo*, can be used similarly by
CC implantation, and the use of the receptor cDNA in gene therapy is

CC also contemplated. Probes based on the cDNA can be used to identify
CC GDNF responsive cells and tissues, e.g., to identify patients who
CC would benefit from GDNF therapy, and abnormalities in receptor
CC expression, and to isolate molecules that form a complex with the
CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
CC antibodies, oligonucleotides derived from the cDNA and animal
CC models that overexpress the receptor can be used to study the
CC biological function of GDNF. Knockout transgenic animals can be
CC used to detect GDNF dependent neurons or processes and the antibody
CC can be used in immunoassays for the receptor. The receptor binds
CC GDNF specifically and with high affinity, acting as part of a
CC complex that mediates/enhances signal transduction by GDNF, i.e.
CC increasing dopamine uptake in dopaminergic cells.
CC Sequence 465 AA;

Query Match	76.38;	Score 1783;	DB 28;	Length 465;
Best Local Similarity	52.88;	Pred. No. 1.15e-157;		
Matches 255: Conservative	25;	Mismatches 185;	Indels 18;	Gaps 0;

D	b	1	mfiatylfahplldlll13aeavsgddr--dcvna5dqclkegascskrytlrlrqvnaqkcl	5
		16	mxllxllslLPLrpxxlLQaELdXgxxRLxXbCvAXXxxxCAEXXCSXXYRTTLROCKAAQvAX	1
Q	y	59	nfa1a5ggleakde--cresama1kqk1lncrcrkrgmkkeknclrlzyswmgylq-qnrl	1
D	b	76	NTYLAAGEXAXXxxXCAAXAXELXXSSLLDCCRCKRGKREXXCLXlYWSXHXHXXGHNX	1
Q	y	116	ledspyer-vnsrlsdllfrvpflsdlvfgqvehlphgncldaaakaculldclckyr5ay	17
D	b	136	LEKSPERPEVY7SRLESDIRRXSXSSXxxXDXDXXXXXSNMCDAAKACNLDNDCKLBRAY	19
Q	y	175	1trpctsvsn-dvcnrrtchak1lqfddkvpakhsygm1fscsr--dlacterrtqltvp	23
D	b	196	IXXCXxxXxxSxERCNRRCRKHALRQFDPKXPHXHYGMLFSCSXxxDXACXERRRQITXP	25
Q	y	232	vcsgyeerhpncldlqgdcctkny1cstr1adfftnqcpaeisvseclkenyadcl1vysg	27
D	b	256	SCSEYEXXKPNCLDLIRXXCRFDLJCRRRLADFTNXXxxXRVVXSXXMXXXC1AAVXG	31
Q	y	292	llgtvmtprvlyds-sls-vapwcdsagnd1leoclklfnfkdnctlknaigafnqs	34
D	b	316	LlETXMTPTMYVDSSTXXAXVAPMCXGSGSNGXABEDECKLDFXXNPPCLXN1QAFNGX	37
Q	y	350	dvrlvwg---pafpqyrttacttaltcalvknkp-19pagsene-1dchv1lppcanlgaqk1	40
D	b	376	XXXXXXXxxXpF5VYXXXXX1XTXAXXVXXXXPSLXXXXSXxxxxLXTVYXXXXXXH1QXQXL	43
Q	y	404	kcnvsgnchlclsn-gnyekegl9aashltckmaapscg1sp1llv1vta1st15lt	46
D	b	436	KXKXSEXXXCXFXELTlTXXXXXSGXXXXXXIXXXXXXXAPXALXPLVPLMTALAXL1SX	49
Q	y	463	ets	465
D	b	496	XXS	498

RESULT	ID	6	W37459 standard; Protein; 460 AA.
AC	W37459;	DT	21-MAY-1998 (first entry)
DE	Human Ret ligand RetL1.		
KM	Ret ligand; RetL; RetL1; receptor; signal transduction; human;		
KM	cell growth; renal cell; nerve cell; renal failure; nephritis;		
KM	kidney transplant; toxic injury; hypoxic injury;		
KM	neurodegeneration; motor neurone disease; multiple sclerosis;		
KM	infection; meningitis; myeloma; Creutzfeldt-Jakob disease;		
KM	cranial nerve injury; spinal cord injury; Down's syndrome;		
KM	cerebral palsy; Lyme disease; muscular dystrophy;		
KM	myasthenia gravis; tumour; therapy.		
OS	Homo sapiens		
PN	MO9744356-R2.		
PD	27-NOV-1997.		
PF	07-MAY-1997; U07726.		

(TM)

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Mpsrch_pp  protein - protein database search, using Smith-Waterman algorithm
Run on:      Mon Mar  8 14:52:02 1999;      MasPar time 24.44 Seconds
Tabular output not generated.              763.226 Million cell updates/sec

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Title: >US-08-866-354-43
Description: (1-498) From US08866354.pep
Perfect Score: 2337
Sequence: 1 MVXXLXXXPYPXXKXKL.....XLPVMTALXLLSXKXS 498
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Scoring table: PAM 150
Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

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Database: plr58
1:plr1 2:plr2 3:plr3 4:plr4
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Statistics: Mean 43.709; Variance 79.332; scale 0.551

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	982	42.0	397	2	JD0082	GPI-linked receptor -	4.74e-19
2	108	4.6	493	2	UC3621	epidermal growth fact	7.35e-03
3	108	4.6	2524	2	A55844	Xtch protein - Atfic	7.35e-03
4	105	4.5	2871	2	A55624	fibroblast 1 precursor	2.04e-02
5	104	4.5	3002	2	JA7221	fibroblast 1 precursor	2.85e-02
6	102	4.4	2871	2	A55567	fibroblast 1 - bovine	5.55e-02
7	97	4.2	1121	2	JO1631	HCRF2 protein - human	2.83e-01
8	97	4.2	3051	2	S42373	hypothetical protein	2.83e-01
9	96	4.1	387	2	I38449	extracellular protein	3.89e-01
10	96	4.1	427	2	DE4813	lybnc protein precursor	5.34e-01
11	95	4.1	1251	2	A57293	latent transforming 9	3.89e-01
12	93	4.0	469	2	A56918	farneoid x-activated	9.98e-01
13	93	4.0	530	2	A31640	epidermal growth fact	9.98e-01
14	94	4.0	879	1	OR071D	ldc receptor precursor	7.31e-01
15	93	4.0	1469	1	B3665	silt protein 2 precu	9.98e-01
16	93	4.0	1480	2	A3665	silt protein 1 precu	9.98e-01
17	93	4.0	2555	2	A40043	notch protein homolog	9.98e-01
18	92	3.9	104	2	JO1757	hypothetical 11.6K pr	1.36e+00
19	92	3.9	200	2	A26637	neurogenic repetitive	1.36e+00
20	92	3.9	259	2	S48713	fetal antigen 1 - hum	1.36e+00
21	92	3.9	260	2	A45549	fetal antigen 1 homoe	1.36e+00
22	90	3.9	312	2	S25708	Olfactory receptor OR	2.51e+00
23	90	3.9	382	2	A37255	serum albumin - bull	2.51e+00

24	92	3.9	383	S53716	homeotic protein dlx	1.35e+00
25	92	3.9	383	B45484	delta-like dlk homeot	1.35e+00
26	90	3.9	565	1 HNN251	hemagglutinin-neurami	2.51e+00
27	91	3.9	826	A50385	monocyte surface anti	1.85e+00
28	92	3.9	832	A12146	neurogenic protein De	1.36e+00
29	92	3.9	833	S19087	gene Delta protein pr	1.35e+00
30	92	3.9	880	S00670	gene Delta protein pr	1.35e+00
31	91	3.9	1232	D64413	notchamin biosynthesi	1.85e+00
32	90	3.9	2531	S18138	notch protein homolog	2.51e+00
33	92	3.9	2907	A17278	fibrillin-2 precursor	1.36e+00
34	92	3.9	2918	A54105	hybridin-2 precursor	1.36e+00
35	89	3.8	249	S09868	hyperthetical protein	3.39e+00
36	88	3.8	384	S25771	gas1 protein - mouse	4.57e+00
37	88	3.8	385	S24785	predilepsy factor 1	4.57e+00
38	89	3.8	509	A49664	activin type I recept	3.30e+00
39	89	3.8	603	S8941	coagulation factor XI	3.39e+00
40	89	3.8	854	1 QHR1YD	LDL receptor precursor	3.39e+00
41	89	3.8	1013	JC2314	chitin synthase (EC 2	3.30e+00
42	89	3.8	1700	S08167	Balbiant ring 3 prote	3.39e+00
43	89	3.8	1712	A28261	masking protein precu	3.39e+00
44	89	3.8	1810	A42230	tenascin precursor -	3.39e+00
45	89	3.8	2471	A49128	cell-fate determinin	3.39e+00

ALIGNMENTS

RESULT	ENTRY	TITLE	ALTERNATE_NAMES	ORGANISM	DATE
1	JEO082	#type complete GPI-linked GPRalpha-3 #formal name Mus musculus 21-Mar-1998	#common_name house mouse		24-Sep-1998

#accession JE0082

#resldues	1-397	##Label	NOM
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COMMENT This protein plays a distinct role in cell survival and

KEYWORDS

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1-25 #domain signal sequence #status predicted #label SIG\
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SUMMARY      #length 397      #molecular-weight 44307      #checksum 2962
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Query match	42.08;	Score 982;	DB 2;	Length 397;
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Matches 157; Conservative 41; Mismatches 194; Indels 26; Gaps 19;

Db 3.LSWSPRPPL-MIL-LVLWLPLG-AGNSLATENRFVNSCTQARKKCEANPACKAYQ 59

[illegible]

[illegible][illegible]


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Db 308 NYVDSPTGIIVSPWPCSGRGSGNMECEKEFLRDTENPCLRNAIOAFNGIDVNVSPKG 367
Oy 324 NYVDSSTXTXXVAPWPCXRGSGNXXEKECEKFLFXNXPCLNAIOAFNGGXXXXXXX 383
Db 368 --PSE-----QA-TQAPREVEKTPSLPDDLSSTSLGTSTVITTCSTVOEGILKANSKEL 418
Oy 384 XXPFSVXXXXXTXTXARVXXXPGLXXXSXKXLLXVXXKXQXKXKXKXKXEX 443
Db 419 SMCFTLTTNITPGSNKVIKPNSGPSRARPSAALTVLVSLMKAL 464
Oy 444 XXCFEELTTNXXKXSGXXXXXXKXKXAPXALXLPVLMLT-AL 488

RESULT 2 PRELIMINARY: PRT: 464 AA.
ID 015328:
AC 015328:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE RET LIGAND 2.
GN RETL2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER:
RX MEDLINE: 97322356.
RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PERINSKY R.B., CATE R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation
RT can be mediated by two different cell-surface accessory proteins.";
RL PROC. NATL. ACADE. SCI. U.S.A. 94:6238-6243(1997).
DR EMBL: U97145; G2282028; -.
SQ SEQUENCE 464 AA: 51543 MW: 28848BD8 CRC32:

Query Match 76.5%; Score 1788; DB 4; Length 464;
Best Local Similarity 56.2%; Pred. No. 0.00e+00;
Matches 262; Conservative 17; Mismatches 166; Indels 21; Gaps 9;

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RESULT 3 PRELIMINARY: PRT: 464 AA.
ID 035977:
AC 035977:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GN GDNF-R-BETA OR RETL2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MORIDAE; MORINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RA TRUPP M., RAYNOSCHER C., IBANEZ C.F.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RX MEDLINE: 97322356.
RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PERINSKY R.B., CATE R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation
RT can be mediated by two different cell-surface accessory proteins.";
RL PROC. NATL. ACADE. SCI. U.S.A. 94:6238-6243(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PERINSKY R.B., CATE R.L.;
RT SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF005226; G2232252; -.
DR EMBL: U97143; G2282024; -.
SQ SEQUENCE 464 AA: 51668 MW: B1A2BD11 CRC32:

Query Match 76.4%; Score 1786; DB 11; Length 464;
Best Local Similarity 56.2%; Pred. No. 0.00e+00;
Matches 262; Conservative 19; Mismatches 164; Indels 21; Gaps 11;

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OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: RODENTIA:
 OC SCURROGNATHI: MORIDAE: MURINAE: MUS.
 RN [1]
 RC STRAIN-C57;
 RA DEY B. K., MONG Y. W., TOO H. P.;
 RL NEUROREPORT 9:0-0(0001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57;
 RA DEY B. K., MONG Y. W., TOO H. P.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF015172; G2624963; -
 SO SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;
 Query Match 73.9%; Score 1727; DB 11; Length 463;
 Best Local Similarity 52.1%; Pred. No. 0.00e+00;
 Matches 249; Conservative 29; Mismatches 178; Indels 22; Gaps 14;
 Db 1 MFLLATYFVLPDLLMAEYSGDRL--DCYKASDQCLKESQSTKRTLRQCYAGKET 58
 16 MFLALSLALPLKXLLQGAELGKXRLXDCVAXXXCXAEXXCYRTLRQCYAGXXX 75
 Db 59 NFSLTSGLKAEDE--CRGAMALKOKSLYNCRCRGMKKEKNCRLTIYMSQSLQ-GNDL 115
 76 NTXLASGEXXKXKXKXAXEXLXSSLYDCRCRGMKKEKXCLTIYMSKXKXKXGKXX 135
 Db 116 LEDSEYED-VNSRLSDIFRAVPEFISV--EHIS--KGNCLDAKACNLDDTCKKRSAY 169
 136 LEXSPYEPXVTSRLSDIFRXXSXXSXXXXXXKXKXCLDAKACNLDDCKLRGAY 195
 Db 170 ITPCTSMNSN-EVCCRRCRCHALROFEDKVPKHSYGLFQSCR--DVACTERRQTIYP 226
 196 IXXCXXKX 255
 Db 227 VCSYERERPNCLNLODSKTYICRSRLADFTNCPESRSVNSCLKENYADCLLAYSG 286
 256 SCSEYKXKRPNCPLDRXXKCRDXLCSRRLADEFTXKXKXKXKXKXKXKXKXKXKX 315
 Db 287 LIGVTMPNYIDS-SLS-VAPWCDSCNSGNDLECLFELNFKDNTCLKNAIQAFNGS 344
 316 LIGVTMPNYDSSKTXKXVAVPWCXKRGSGXKXKXKXKXKXKXKXKXKXKXKXKX 375
 Db 345 DVTMQRPA--P--PVOTTTATTTAFRIKMP-LCPASSENE-ITHTVLPCCANTQAOKL 398
 376 XXXXXXXXXKX 435
 Db 399 KSNVSGSTHLCSDNDYGRKDLGASSHITTKSMAPPSCGLSSPVAVFTALALLS 456
 436 KXNKSXKX 493
 RESULT 9 PRELIMINARY: PRT: 431 AA.
 AC 093512;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GFR RECEPTOR ALPHA 4 PRECURSOR.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: ARCHOSAURIA: AVES;
 OC NEOGNATHAE: GALLIFORMES: PHASIANIDAE: PHASIANINAE: GALLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 98313402.
 RA THOMPSON J., DOXAKIS E., PINON L. G., STRACHAN P., BUO-BELLO A.,
 WYATT S., BUCHMAN V. L., DAVIES A. M.;
 RT "GFRalpha-4, a new GDNF family receptor";
 RL MOL. CELL. NEUROSCI. 11:117-126(1998).
 DR EMBL: AF045162; G2906032; -
 KW SIGNAL.
 FT SIGNAL. 1 17 POTENTIAL.

FT CHAIN 18 431 GFR RECEPTOR ALPHA 4.
 SO SEQUENCE 431 AA; 47964 MW; 7AE1F0BD CRC32;
 Query Match 52.1%; Score 1218; DB 13; Length 431;
 Best Local Similarity 45.9%; Pred. No. 2.58e-262;
 Matches 157; Conservative 39; Mismatches 132; Indels 14; Gaps 9;
 Db 25 DCLGAGSCTNDPICSSKFRTRLROCIAGNGANK-L--GPDANK--CRSYTALLSOLY 79
 45 DCVAXKX 104
 Db 80 GCKCRGMKKEKNCLEYSYWIHTLMGEMNVLSESPPEPIRG-F-DYVRLASTAGSEN 137
 105 DCRCKRGMKKEKNCLEYSYWIHTLMGEMNVLSESPPEPIRG-F-DYVRLASTAGSEN 164
 Db 138 EVTGV---NRCCLDAKACNDKEMCQRLTEYVSCFIRRLRADTCNRSKCHALRKFDR 194
 165 DXXKX 224
 Db 195 VPPEYTHLEFQCE--DIAEERRRQTIYPACSEKESKRNCLAPLDSRENVVCRSRY 252
 225 VPXXKX 284
 Db 253 AEFQNCPSLOTASGCRSDSYACILATYGIISPTTPYIDRS-TSS-IAPYCTGNAS 310
 285 ADFXTNCKX 340
 Db 311 GNRQECESFLHFTDVCCLONAIQAFNGTYLNAATAPSS 352
 345 GXXKX 386
 RESULT 10 PRELIMINARY: PRT: 400 AA.
 AC 060609;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE GDNF FAMILY RECEPTOR ALPHA 3.
 GN GFR3.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: PRIMATIA:
 OC CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BALOH R. H., GORODINSKY A., GOLDEN J. P., TANSEY M. G., KECK C. L.,
 RA POBESCU N. C., JOHNSON E. M. JR., MILBRADT J.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
 DR EMBL: AF051767; G2961632; -
 SO SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;
 Query Match 43.9%; Score 1027; DB 4; Length 400;
 Best Local Similarity 37.1%; Pred. No. 4.39e-215;
 Matches 156; Conservative 47; Mismatches 195; Indels 23; Gaps 17;
 Db 1 MYRLNRPRLPVPVTLMLLLPLPS-PLPLA-AGDPLTESRLNMSCLOARRKCOADPTCS 58
 1 MYXKX 60
 Db 59 AAYHHLDSCTSI--STPLPS-EEPSVPADCLEAQQRLNSSLGCGCHRRMRNOVACLD 115
 61 XXYITLROCAKX 120
 Db 116 IYTVHARSLSGNYELDVSPEDYVTSK-P--WRM-NL-SKL--NMLKPD--SDCLKLFAM 167
 121 IYVXKX 180
 Db 168 LCTLNKCDRLKRAYGKAC---SGP-HCQRHVCRLRLTFEFAEPHAGLLCPCAP 222
 181 ACNINDCKRLRSAYIXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 240
 Db 223 NDRCGERRNTIAPNCLALPVA--PNCLTLRLCFSPDLCSRVDVDTCHPHMD-ILGT 280

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OY 241 XDAXCERRROTIXPSCSYEXXKPNCLDLRXXCORTDLCRSRLADEXTNCGXXXXXXVXS 300
Db 281 CATEO--SRCRAYLGLIGTAMTPNFV--SNVNTS--VALSTCRGSGNQECECMLEGFESH 337
OY 301 CAXANXXCCLAXXGLIGTAMTPNYVDSXTXXVAVWCRCRSGNKECEKFLXFFXX 360
Db 338 NPLTEAIAAKMRFHQSOLFQDWPHPFVAVMAHQENPAVRPQWPVPSLFCSTLPLILL 397
OY 361 NPLCAXNAIQAFNGNGXXXXXXPPFSVXXXXXTTAXARVXXSLAXXXXXXXLX 420
Db 398 S 398
OY 421 T 421

RESULT 11
ID 055243 PRELIMINARY: PRT: 397 AA.
AC 055243:
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
RT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
RT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFR3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENFALK J., TOMAC A., LINDQVIST E., HOFFER B., OLSON L.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RA NAVELIHAN P., BAUDET C., MIKAEIS O., SHEN L., WESTPHAL H., ENNFORS P.;
RP SEQUENCE FROM N.A.
RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1997).
DR EMBL: AF041842; G2921579; -
DR EMBL: AF036163; G2674177; -
SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 42.0%; Score 982; DB 11; Length 397;
Best Local Similarity 37.6%; Pred. No. 5, 266-204;
Matches 157; Conservative 41; Mismatches 194; Indels 26; Gaps 19;

Db 3 LSLERPPPLL-MIL-LTVLSLWPLG-AGNSLATERNFVNSTQARKKEANPACKAAVQ 59
OY 5 LXXXPPXXMXKLXSLALPLXXXLQGAELGXKRLXDCVAXXKXAXXCSXXR 64
Db 60 HIGSTSSLSR--PLPL--EESAMSDCLEAAEQLNSSLIDCRCHRMKHOATCIDIYT 116
OY 65 TLROCXAGXXNXTXLASGEXXXXXXXCXAXEXLXXSSLYDCRCRGMKEXXCLXIYWS 124
Db 117 VPARSLGDYELDVSPYEDTVTSK--P--WKM-NL-SKL--NMLKPD--SDLCFKFAMLC 168
OY 125 XHXXLXGXKXLEKSPYEVYTSRLSDIFRXXSXKXKXKXKXKXKXKXKXKXKXKXKX 184
Db 169 HDKCDRLKRAYEAC-----SGI-RCORHLCIAQLRSFEKAEASHAOGLLCPCEPDAG 223
OY 185 NDCKRLRSAYIXKXXXXXXKXERCNRRKCHALRQFEDKVPXHXHYGMLFCSCAXXDXA 244
Db 224 CGERRNTIAASCALPSV--TPNCLDLRSFCRADPLCRSLMDFOTHCPMD--ILGTCA 281
OY 245 CXERRROTIXPSCSYEXXKPNCLDLRXXCORTDLCRSRLADEXTNCGXXXXXXVXS 304
Db 282 Q-SRCLRAYLGLIGTAMTPNF--SKVNTVALSCTCGSGNLDCEQLEERSQNPCL 338
OY 305 NYXKCLAXYXGLIGTAMTPNYVDSXTXXVAVWCRCRSGNKECEKFLXFFXXNPCL 364
Db 339 VEALIAAKMRFHQSOLFQDWPHPFVAVMAHQENPAVRPQWPVPSLFCSTLPLILL 395
OY 365 XNAIQAFNGNGXXXXXXPPFSVXXXXXTTAXARVXX--PSLXXXXXXKXKXKXLT 421

RESULT 12
ID 035118 PRELIMINARY: PRT: 397 AA.

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AC 035118;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA 3
DE (GFRALPHA-3).
GN GFR3 OR GFRALPHA-3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL6; TISSUE-HEART;
RX MEDLINE: 98205811.
RA NOMOTO S., ITO S., YANG L.-X., KIUCHI K.;
RT "Molecular cloning and expression analysis of GFR alpha-3, a novel
RT cDNA related to GDNF alpha and NTN alpha."
RL BIOCHEM. BIOPHYS. RES. COMMUN. 244:849-853(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA BALCH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
RA POPESCU N.C., JOHNSON E.M., JR., MILBRANDT J.;
RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
DR EMBL: AB008833; D1024441; -
DR EMBL: AF051766; G2961630; -
DR MGD: MGI:1201403; GFR3.
SQ SEQUENCE 397 AA; 44307 MW; AB0ED024 CRC32;

Query Match 42.0%; Score 982; DB 11; Length 397;
Best Local Similarity 37.6%; Pred. No. 5, 266-204;
Matches 157; Conservative 41; Mismatches 194; Indels 26; Gaps 19;

Db 3 LSWSPRPLL-MIL-LTVLSLWPLG-AGNSLATERNFVNSTQARKKEANPACKAAVQ 59
OY 5 LXXXPPXXMXKLXSLALPLXXXLQGAELGXKRLXDCVAXXKXAXXCSXXR 64
Db 60 HIGSTSSLSR--PLPL--EESAMSDCLEAAEQLNSSLIDCRCHRMKHOATCIDIYT 116
OY 65 TLROCXAGXXNXTXLASGEXXXXXXXCXAXEXLXXSSLYDCRCRGMKEXXCLXIYWS 124
Db 117 VPARSLGDYELDVSPYEDTVTSK--P--WKM-NL-SKL--NMLKPD--SDLCFKFAMLC 168
OY 125 XHXXLXGXKXLEKSPYEVYTSRLSDIFRXXSXKXKXKXKXKXKXKXKXKXKXKXKX 184
Db 169 HDKCDRLKRAYEAC-----SGI-RCORHLCIAQLRSFEKAEASHAOGLLCPCEPDAG 223
OY 185 NDCKRLRSAYIXKXXXXXXKXERCNRRKCHALRQFEDKVPXHXHYGMLFCSCAXXDXA 244
Db 224 CGERRNTIAASCALPSV--TPNCLDLRSFCRADPLCRSLMDFOTHCPMD--ILGTCA 281
OY 245 CXERRROTIXPSCSYEXXKPNCLDLRXXCORTDLCRSRLADEXTNCGXXXXXXVXS 304
Db 282 Q-SRCLRAYLGLIGTAMTPNF--SKVNTVALSCTCGSGNLDCEQLEERSQNPCL 338
OY 305 NYXKCLAXYXGLIGTAMTPNYVDSXTXXVAVWCRCRSGNKECEKFLXFFXXNPCL 364
Db 339 VEALIAAKMRFHQSOLFQDWPHPFVAVMAHQENPAVRPQWPVPSLFCSTLPLILL 395
OY 365 XNAIQAFNGNGXXXXXXPPFSVXXXXXTTAXARVXX--PSLXXXXXXKXKXKXLT 421

RESULT 13
ID 035325 PRELIMINARY: PRT: 397 AA.
AC 035325;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFR3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]

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CC relates to native rat GDNF alpha (see W27327), its variants and
 CC soluble derivatives (extracellular domain), chimeric GDNF alpha
 CC and antibodies which bind to the GDNF alpha, including agonist
 CC and neutralising antibodies, as well as various uses for these
 CC molecules. It also relates to assay systems for detecting ligands
 CC to GDNF alpha, systems for studying the physiological role of
 CC GDNF, diagnostic techniques for identifying GDNF-related conditions,
 CC methods for identifying molecules homologous to GDNF alpha, and
 CC therapeutic techniques (claimed) for the treatment of GDNF-related
 CC and GDNF alpha-related conditions, particularly kidney disease
 CC associated with glomerulonephritis and enteric nervous system
 CC related disorders. Transgenic and knockout animals are also
 CC claimed.
 CC Sequence 468 AA:

Query Match 85.0%: Score 1779; DB 27; Length 468;
 Best Local Similarity 50.7%: Pred. No. 2,89e-167;
 Matches 241; Conservative 12; Mismatches 213; Indels 9; Gaps 8;

3 laltfajlplldlmsaevsgdrlcdvksadqclkegsctkyrtlrgcvaqketnfsal 62
 15 LXTLXSLXPLXLLXSSXXXXXDXVAXXAXXCAEXXCSXXYRTLQCAAGXXXXX 74
 Db 63 tsjleakdecrsamalqkqsljncrcrkymkknclrljwsmysqslq-gndlledsdy 121
 Oy 75 XXXXXAXXEXXAXEXLXXSSLYDCRCKRGMKEXXCLXLYWSXHXLLXGXXXLEXSPY 134
 Db 122 e-pvnsrlsdiffrvplfsdvfgqvehlskgnncldaaacnldctckkyrsayltptctt 180
 Oy 135 EXPVTSRLSDIFRXXSXSSXXXXXDXVAXXAXXCAEXXCSXXYRTLQCAAGXXXXX 194
 Db 181 smsn-evcnrrkchkalqfifdkvpahkshygmllfscsr--diacterrirglvpcvsyee 237
 Oy 195 XXSXXERCNRKCHALRQFEDKVPXHXHYGMFLFCSCXXDXACXERRRQTIYPCSCYEX 254
 Db 238 reipncisldgscctnylrcsrldaffncqpearsvsnclkenyadcllaysgllgtvm 297
 Oy 255 XEXPNCIDLRXCRTRDLCRSRLADFTXNCXPRXRXRXCXKXNXXCXLMXVXGLIGTXM 314
 Db 298 tpmvdsas-sls-vapwcdsgnsqndledclkfnnfkdntclknalgaifgnsdvrtmq 355
 Oy 315 TPNVDSAXTXXXVAPWCDSGNSGNGXEECEKFLXFXNPLNMAIOAFGNGXDVXMSQ 374
 Db 356 paprvqtltatcttafrvknkp-1pgagsene1p-thvlppcanlgaqklkxnvsgsthl 413
 Oy 375 XXPXXXTXAXXXXXRVXXXPXLLXXSSXXXXTVXXXXQXQXKXNXXSXXX 434
 b 414 clsdedfgkdgagashltkmaappscslslpvlmltalael1svslaets 468
 Oy 435 CXXXXXXSXXXXXXSXXXXXXSXXLXLPVLMLETLXKXLLXKXLEXETS 489

RESULT 2
 ID W35334 standard: Protein: 468 AA.
 AC W35334;

DT 01-MAY-1998 (first entry)
 DE Rat glial cell line-derived neurotrophic factor receptor.
 KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.
 OS Rattus sp.
 PN M09740152-A1.
 PD 30-OCT-1997.
 PE 15-APR-1997; U06281.
 PR 14-APR-1997; US-837199.
 PR 22-APR-1996; US-015907.
 PR 09-MAY-1996; US-017221.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI, 97-535836/49.
 DR N-PSDB: T95297.

PT glial cell line derived neurotrophic factor receptor - useful to
 PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and
 PT Alzheimer's disease
 PS Claim 1; Pages 96-98; 196pp; English.
 CC The present sequence is the rat glial cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or amyotrophic lateral sclerosis, complications of diabetes
 CC and Huntington's disease and (optionally in combination with GDNF)
 CC glaucoma, retinal degeneration and hearing loss caused by injury to
 CC inner ear sensory neurons. The receptor can also be used to block
 CC unwanted GDNF activity, analyse GDNF related molecules and
 CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
 CC cells, preferably transfected ex vivo, can be used similarly by
 CC implantation, and the use of the receptor cDNA in gene therapy is
 CC also contemplated. Probes based on the cDNA can be used to identify
 CC GDNF responsive cells and tissues, e.g. to identify patients who
 CC would benefit from GDNF therapy, and abnormalities in receptor
 CC expression, and to isolate molecules that form a complex with the
 CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
 CC antibodies, oligonucleotides derived from the cDNA and animal
 CC models that overexpress the receptor can be used to study the
 CC biological function of GDNF, knockout transgenic animals can be
 CC used to detect GDNF dependent neurons or processes and the antibody
 CC can be used in immunoassays for the receptor. The receptor binds
 CC GDNF specifically and with high affinity, acting as part of a
 CC complex that mediates/enhances signal transduction by GDNF, i.e.
 CC increasing dopamine uptake in dopaminergic cells.
 CC Sequence 468 AA:

Query Match 85.0%: Score 1779; DB 28; Length 468;
 Best Local Similarity 50.7%: Pred. No. 2,89e-167;
 Matches 241; Conservative 12; Mismatches 213; Indels 9; Gaps 8;

3 laltfajlplldlmsaevsgdrlcdvksadqclkegsctkyrtlrgcvaqketnfsal 62
 15 LXTLXSLXPLXLLXSSXXXXXDXVAXXAXXCAEXXCSXXYRTLQCAAGXXXXX 74
 Db 63 tsjleakdecrsamalqkqsljncrcrkymkknclrljwsmysqslq-gndlledsdy 121
 Oy 75 XXXXXAXXEXXAXEXLXXSSLYDCRCKRGMKEXXCLXLYWSXHXLLXGXXXLEXSPY 134
 Db 122 e-pvnsrlsdiffrvplfsdvfgqvehlskgnncldaaacnldctckkyrsayltptctt 180
 Oy 135 EXPVTSRLSDIFRXXSXSSXXXXXDXVAXXAXXCAEXXCSXXYRTLQCAAGXXXXX 194
 Db 181 smsn-evcnrrkchkalqfifdkvpahkshygmllfscsr--diacterrirglvpcvsyee 237
 Oy 195 XXSXXERCNRKCHALRQFEDKVPXHXHYGMFLFCSCXXDXACXERRRQTIYPCSCYEX 254
 Db 238 reipncisldgscctnylrcsrldaffncqpearsvsnclkenyadcllaysgllgtvm 297
 Oy 255 XEXPNCIDLRXCRTRDLCRSRLADFTXNCXPRXRXRXCXKXNXXCXLMXVXGLIGTXM 314
 Db 298 tpmvdsas-sls-vapwcdsgnsqndledclkfnnfkdntclknalgaifgnsdvrtmq 355
 Oy 315 TPNVDSAXTXXXVAPWCDSGNSGNGXEECEKFLXFXNPLNMAIOAFGNGXDVXMSQ 374
 Db 356 paprvqtltatcttafrvknkp-1pgagsene1p-thvlppcanlgaqklkxnvsgsthl 413
 Oy 375 XXPXXXTXAXXXXXRVXXXPXLLXXSSXXXXTVXXXXQXQXKXNXXSXXX 434
 b 414 clsdedfgkdgagashltkmaappscslslpvlmltalael1svslaets 468
 Oy 435 CXXXXXXSXXXXXXSXXXXXXSXXLXLPVLMLETLXKXLLXKXLEXETS 489

RESULT 3
 ID W37457 standard: Protein: 468 AA.
 AC W37457;

DT 21-MAY-1998 (first entry)
 DE Rat Ret ligand RetL.
 KW Ret ligand; RetL; RetL; receptor; signal transduction; rat;

KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /Label= Sig-peptide
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00245.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 49-51: 113pp: English.
 CC This protein comprises rat Ret ligand (RetL, RetL1, a key component
 CC of the Ret signalling pathway that specifically interacts with Ret
 CC receptor protein, triggering Ret dimerisation and/or
 CC autophosphorylation of the Ret tyrosine kinase domain. The amino
 CC acid sequence was deduced from a cDNA clone (see V00245) obtained
 CC from a rat embryonic kidney cDNA expression library. Human RetL1
 CC as well as mouse and human RetL2 and RetL3 sequences have also been
 CC identified (see W37458-63). Vectors containing RetL1 DNA and
 CC prokaryotic or eukaryotic host cells transformed or transfected
 CC with these vectors are claimed, as well as a method for production
 CC of RetL1, its soluble variants (e.g. amino acids 1-434) and fusion
 CC proteins with a toxin, imageable compound or radionuclide. RetL1,
 CC optionally when expressed from vectors in vivo, is used to promote
 CC growth of new tissue and survival of damaged tissue, particularly
 CC kidney or neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 468 AA;
 Query Match 85.0%; Score 1779; DB 28; Length 468;
 Best Local Similarity 50.7%; Pred. No. 2, 89e-167;
 Matches 241: Conservative 12; Mismatches 213; Indels 9; Gaps 8;

Db 238 reipncslgdcstnylcrsladffncgpeersvsnclkenyadcllayagslgvtm 297
 | ||||| : ||| : ||||| ||||| : ||| : ||||| ||||| : ||||| : ||||| :
 Oy 255 XEPCNCDLRSXCRDXLCRSLADFTKNCXPRXXRTXCAAXVXXCLXAYXGLIGTM 314
 Db 298 tpmvds-sls-vapwcdsngndledclftnfkdntclnaqlafongsdvtmvg 355
 | ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
 Oy 315 TPNVYDSXRTXXVAPWCXRGSGNXXECCFKLXPFXXNCLXNAIOAFNGXDXMKS 373
 Db 356 papvgttattctafvknkp-igpagsenelp-thvlpccanlgqklsnvssthl 4
 | ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
 Oy 375 XXPXXXTXAXXXXXRXVXXPXXLXXXXXXXTXXXXXXXXQXXQXXLXXNXXSAXXX 4
 Db 414 clsdadfgkglagasshlttsmaappscslsajpvlmltalaisvsiaets 468
 | ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
 Oy 435 CXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXHXXH 489
 RESULT 4
 ID W37460 standard; Protein; 464 AA.
 AC W37460:
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL2.
 KW Ret ligand; RetL; RetL2; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00248.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 69-70: 113pp: English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL2,
 CC deduced from a cDNA clone (see V00248) isolated from a human foetal
 CC liver library. Rat and human RetL1 and human and mouse RetL3
 CC sequences (see W37457-59 and W37461-63) are also claimed. Human
 CC RetL2 is 49.1% identical to human RetL1 protein. RetL1 is a
 CC key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL2 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL2, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL2, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 464 AA;

Query March 84.58; Score 1768; DB 28; Length 464;
Best Local Similarity 53.38; Pred. No. 3,906-166;
Matches 244; Conservative 14; Mismatches 187; Indels 13; Gaps 4;

```
Db      16 tlrslaspsalqgpelhwprpvdcranelaaeencsaryrltgrclagrdntml-- 73
Oy      17 TLXSLXPLXPLXSSXXXXXXXDXVAXXXXCKAEKSSXXRTLRGCKXAGKXNXXXXX 76
Db      74 ---ankecgaaalelqesplydcrcrkgrmkkelqclqylwslhlylgtgeefyaape- 129
Oy      77 XXXAXXECXAXXEXLXXSSLYDCRCRGRKKEXCLXLYWSXHXLLXGXXXXLEXPFX 136
Db      130 pvtcrslsdftrlasifsgcgadpovvsakenhldaaacnlnndocklrssylcmrel 189
Oy      137 PVTSRSLSDIFRXXSSXXSXDXDXXXXXSNMCLDAKACNINDCKRTKSAYIXXCKXXX 186
Db      190 spfercnrrckhalkqifdaryseyetymlfscsq--dqcaertrqtlpsscvedke 247
Oy      197 SXXERCNRRCXKHALQGFDDKVPXHXHYGMLESCXDXDADACERRRQTIIPSCSYXXE 256
Db      248 kmncldlrgvctrdhlcrrsladfnacraasyqvtscpadnyacilsgyagmgidfamp 307
Oy      257 XPNCPLDRSXCRDTDLXCRSLADFYTNCPXRXXTXCKAXXNYXCKLAXXAGLIGTMT 316
Db      308 nnydsapgilvqpwscscrgsgmmeecokfirdtempclrnaiaqafngtdnvspkg 367
Oy      317 NYDSXXTXXXVAPWCKSGSNNXXEECEKFLXFXKNPCIXNAIOAFGNGXDVMXQXX 376
Db      368 psfqatqap-----rvetktpsfpddlsdstslgtsvltctsvgegljkansekmsmf 422
Oy      377 PXXXXTXAXXXXXXNRXXXXPLXXXXXXNXTYVXXCKXKXOXKXLNKXSKXXXXX 436
Db      423 teltnllpgsnkvlkpnsgparpsaalvslavlml 460
Oy      437 XXXXXXXXXXXXXXXXXXXXXXXXKXAXXSLXXLLPLML 474
```

RESULT 5

ID W35333 standard; Protein; 465 AA.

AC W35333:

DT 01-MAY-1998 (first entry)

DE Human glial cell line-derived neurotrophic factor receptor.

KW Human glial cell line-derived neurotrophic factor; GDNF; receptor; treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; diabetes; Huntington's disease; glioma; retinal degeneration; hearing loss; gene therapy.

OS Homo sapiens.

PN MO9740152-A1.

PD 30-OCT-1997.

PF 15-APR-1997; 006281.

PR 14-APR-1997; US-837199.

PR 22-APR-1996; US-015807.

PR 09-MAY-1996; US-017221.

PA (AMGE-) AMGEN INC.

PI Fox GM, Jing S, Wen D;

WP1: 97-55856/49.

DR N-PSDB: 188419.

PT Glial cell line derived neurotrophic factor receptor - useful to treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's disease.

PS Claim 1: Pages 91-93; 196pp. English.

CC The present sequence is the human glial cell line-derived neurotrophic factor (GDNF) receptor, which can be used to treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's disease or amyotrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally in combination with GDNF) glioma, retinal degeneration and hearing loss caused by injury to inner ear sensory neurons. The receptor can also be used to block unwanted GDNF activity, analyse GDNF related molecules and stabilise GDNF in pharmaceutical formulations. Receptor expressing cells, preferably transfected ex vivo, can be used similarly by implantation, and the use of the receptor cDNA in gene therapy is

CC also contemplated. Probes based on the cDNA can be used to identify CC GDNF responsive cells and tissues, e.g. To identify patients who would benefit from GDNF therapy, and abnormalities in receptor expression, and to isolate molecules that form a complex with the cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor antibodies, oligonucleotides derived from the cDNA and animal models that overexpress the receptor can be used to study the biological function of GDNF. knockout transgenic animals can be used to detect GDNF dependent neurons or processes and the antibody can be used in immunoassays for the receptor. The receptor binds GDNF specifically and with high affinity, acting as part of a complex that mediates/enhances signal transduction by GDNF, i.e., increasing dopamine uptake in dopaminergic cells.

SQ Sequence 465 AA:

Query Match 81.0%; Score 1695; DB 28; Length 465;
Best Local Similarity 49.5%; Pred. No. 1,236-158;
Matches 235; Conservative 17; Mismatches 211; Indels 12; Gaps

D 3 lallfaplpjlllisaevgsdrlidcvkaadgclkegscstkyrtlrqcaagketfsi
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
15 LMTLKLXPLRLKLSXXXXXXDCVAXXXXCAEEXCXRTTLROCKAGGXXXXXX 74
D 63 asgleakdecrsamealkqkslyncrcrkgmkkehcnlrytswyga1q-gndiledspy 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
75 XXXXXXKXCXAXEXLXSSLYDRCRKGMKEXXCLXIYWSHXHXLXGXKXLEKSPY 134
D 122 e-pvnsrlsdfrvvpflsgdrfqgehlphkgnncldaekenldickkyrsayltprct 160
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
135 EXPVTSTRISDLIRFXSXSXXXXDXKXXXXKSNCLDAKACNLMDCKKRISAIVIXCXX 194
D 181 svsn-dvcnrrckchkalrqfdkypahskysmifcscr--diacterrigtlypvcsye 237
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
195 XSXSEKRCNRCHALNQFDKNPXXHXHYMLSCSXKXDMAKEXERRTIPSCSYEX 254
D 238 rdkpnclnlgdccknyicrsrlsdffncqesrsvscklenyadcllaysgllgtvm 297
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
255 KXPFCDLRSICRDMLCRSRLDFTNCPXXRXXTXCAXNVXXCLAAVYGLLGTVM 314
D 298 tpmvldas-sls-vavpcdcensgndleecikfnffkdntcihnalgaefngsgdvctvw 355
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
315 TPNIYDSXITXXVAAPMCXRGSGNXEBCEKFLEXXXNPCLLNATOAFGNGXDVMGSO 374
D 356 pafpwqttaettatlvknkp-lpgpseneip-thvlppcanlaqaqlksnvsgnthl 413
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
375 XXPXKXITAXXXXXRRYXXPXLIXXXXXXXTGVXXXXCXXOXQLKKNXKXXXXX 434
D 414 clsmngnyekeglgashltck-smaappscglpllylvvtalstils--lets 465
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
435 CAXXXXXXXXXXXXXXXXXXXKAXXSLXLLPVLMLTXLXLLXLLXLETTS 489

RESULT 6
ID W37459 standard; Protein: 460 AA.
DC W37459:
DE 21-MAY-1998 (first entry)
DE Human Ret Ligand Recl1.
RW Cell growth; Ret1; receptor; signal transduction; human;
RW cell ligand; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebellar palsy; Lyme disease; muscular dystrophy;
MS myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN MO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; D07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.

PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 N-PSDB: V00247.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 64-66; 113pp. English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL,
 CC deduced from cDNA clones (see V00247) isolated from a human
 CC foetal kidney. RetL and mouse and human RetL2 and RetL3
 CC sequences (see W37457 and W37460-63) are also claimed. The
 CC human RetL sequence is 93.3% identical to that of rat. RetL
 CC is a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor, triggering Ret dimerisation and/or
 CC autophosphorylation of the Ret tyrosine kinase domain. Vectors
 CC containing RetL DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of RetL, its soluble variants and fusion
 CC proteins with a toxin, imageable compound or radionuclide. RetL,
 CC optionally when expressed from vectors in vivo, is used to promote
 CC growth of new tissue and survival of damaged tissue, particularly
 CC kidney or neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 460 AA.

Query Match 78.6% Score 1644; DB 28; Length 460;
 Best Local Similarity 49.5% Pred. No. 2,11e-153;

Matches 235; Conservative 17; Mismatches 206; Indels 17; Gaps 12;

DB 3 latlyfalplldllsaevsggrldcvkasdqckegscstkyrtlrqcvagketnfal 62
 15 LKTLKSLXPLXKX 74
 DB 63 aaglekdcrcsmaealkqkslyncrcrkmkckncllywmysglq-gndllsdpy 121
 75 KX 134
 DB 122 e-pvnsrlsdlffvvpfisy---ehlp--kgnncldaakacnldldckkyrsaylpcpt 175
 135 KXPVTRSLDIFKX 194
 DB 176 vswn-dvcnrtkckhalrgffdkvpakhsygmfcscr--diacterrtqtlypvcys 232
 195 KX 254
 DB 233 rekpnclnlgdscktnylcstrladdffncqpsrsvssclkenygdcllysgqllgtm 292
 255 XEKPNCILDRSKCRTDXLCRSRLADXYTNCXPXKXKXKXKXKXKXKXKXKXKXKX 314
 DB 293 tpmvldss-sls-vapwcdcsnsgndleelckfnnfkntclknalgaifgnsdvtvng 350
 315 TPTVYVSXKTXKX 374
 DB 351 pafvgttatttaltatvknkp-lspagenealp-chviprcanlgaqklknvsgnchl 408
 375 KXPXKX 434
 DB 409 clsnngykegagashltck-smaapscgslpilylvtaltstls--ltets 460
 435 CXKX 489

RESULT 7

ID W37458 standard; Protein: 346 AA.
 AC W37458;
 DT 21-MAY-1998 (first entry)
 DE Human Ret Ligand RetL1 partial sequence.
 KW Ret Ligand; RetL; RetL1; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 N-PSDB: V00246.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 60-61; 113pp. English.
 CC This amino acid sequence comprises a human Ret ligand (RetL) RetL
 CC partial polypeptide sequence, deduced from a partial clone (see
 CC V00246) isolated from a human embryonic kidney cDNA library. a
 CC full-length RetL sequence (see W37459) is also claimed, as well
 CC as rat RetL and mouse and human RetL2 and RetL3 sequences (see
 CC W37457 and W37460-63). RetL is a key component of the Ret
 CC signalling pathway that specifically interacts with Ret receptor
 CC protein, triggering Ret dimerisation and/or autophosphorylation of
 CC the Ret tyrosine kinase domain. Vectors containing RetL DNA and
 CC prokaryotic or eukaryotic host cells transformed or transfected
 CC with these vectors are claimed, as well as a method for production
 CC of RetL, its soluble variants and fusion proteins with a toxin.
 CC Imageable compound or radionuclide. RetL, optionally when
 CC expressed from vectors in vivo, is used to promote growth of new
 CC tissue and survival of damaged tissue, particularly kidney or
 CC neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 346 AA.

Query Match 60.0% Score 1255; DB 28; Length 346;
 Best Local Similarity 51.0% Pred. No. 1,41e-113;

Matches 184; Conservative 16; Mismatches 145; Indels 16; Gaps 11;

DB 2 ledspye-pvnsrlsdlffvvpfisy---ehlp--kgnncldaakacnldldckkyrsay 5
 129 LEXSPYEVTRSLDIFKX 174
 DB 56 lrpctsvsn-dvcnrtkckhalrgffdkvpakhsygmfcscr--diacterrtqtlyp 10
 189 KX 172
 DB 113 vcsyeerkpnclnlgdscktnylcstrladdffncqpsrsvssclkenyadcllysg 172
 249 SCSEYEXKX 308
 DB 173 lgtvmtpmvldss-sls-vapwcdcsnsgndleelckfnnfkntclknalgaifgns 230

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OY 309 LGTMTPTVYDSXXVAVPMCKRGSGNXXECEKFLXXFXNPLXNIQAFGNXX 368
DB 231 dvtvqpaipvtctattcttaltvknkp-1gpaageenelp-thvlpccanlqaklksnv 288
OY 369 DVMXSOQXFXPXXXTXAXXXXXXXRVXXXPYLXXXSXXXXXXVXXXCXXOXLKKNX 428
DB 289 sgntnlclsnngykekeglgashlctk-smaapscqglplvlvtaltstlls--1let 345
OY 429 SXXXXXXCXXXXXXSXXXXXXSXXXXXXSXXXXXXSXXXXXXSXXXXXXSXXXXXX 488
DB 346 s 346
OY 489 S 489

RESULT 8
ID W37461 standard; Protein: 397 AA.
NC W37461;
NC 21-MAY-1998 (first entry)
KW Mouse Ret. ligand RetL3.
KW Ret. ligand: RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Mus musculus.
PN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997: U07726.
PR 10-APR-1997: US-017427.
PR 08-MAY-1996: US-017427.
PR 07-JUN-1996: US-019300.
PR 16-JUL-1996: US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
PI WPI: 98-018431/02.
DR N-PSDB: V00249.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2: Page 77-78; 113pp; English.
CC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,
CC deduced from cDNA clones (see V00249) isolated from an EST
CC database and by 5'RACE. Rat and human RetL1, human RetL2 and RetL3
CC sequences (see W37457-60 and W37462-63) are also claimed. RetL is
CC a key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
CC cells transfected or transfected with these vectors are claimed, as
CC well as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue.
CC Particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.
SQ Sequence 397 AA;

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Query Match 46.7%; Score 976; DB 28; Length 397;
 Best Local Similarity 40.4%; Pred. NO. 3.53e-85;

```

Matches 143; Conservative 35; Mismatches 157; Indels 19; Gaps 1.
DB 10 p1m11111v1w1p1p1gag1nat1en1fvn1a1c1t1a1r1k1t1c1e1a1n1p1a1q1h1s1c1t1s1s 69
OY 10 PXXXXLXLTLSLXPLXPLXLSXSSXXXXXXDXCVAXXXCNAEXXCSXXVRLTRCCKXGXX 69
DB 70 rplpleesamaa-dcleaeag1lms1ldcrchrnmkqg1cld1y1w1v1p1a1r1s1g1d1e1l 126
OY 70 XNXXXXXXAXXAXXECXAXXEXLXSSLYDCCKRGKMKEXXCLTIYXSHXAXLXGXXXL 129
DB 129 dvsyedtvtak-p--wkm-nl-skl--nm1kpd-sd1cl1fam1c1t1h1k1cd11r1k1ay1g 180
OY 130 EXPPEXPEVTSRLSDIFRXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXX 189
DB 181 eac-----sgt-rqqrh1claq1r1f1e1k1a1e1s1h1g1l1l1c1p1a1d1a1g1c1e1r1n1t1a1p1s 235
OY 190 XXXXXXXXXEXRCKNRKHKALROFFDKVPYXXHYGM1FCSCXXXDXNACXERRRQ1T1XPS 249
DB 236 calpsv-tpncld1rsfcradp1crsr1mdftq1chmd1lgt-cateq-srclray1g1 292
OY 250 CSEYEXXEPNCLDRSKCRTX1LRSRLADPXTXCYPXRXXT1CXAXN1YXXCLXATXG1 309
DB 293 1gtamtptfiskvnt--val1sc1cr1sg1n1q1d1c1e1q1e1r1s1f1s1q1n1p1l1v1e1a1a1 344
OY 310 IGTMTPTVYDSXXVAVPMCKRGSGNXXECEKFLXXFXNPLXNIQAFGNXX 363

RESULT 9
ID W37463 standard; Protein: 400 AA.
NC W37463;
NC 21-MAY-1998 (first entry)
KW Human Ret. ligand RetL3.
KW Ret. ligand: RetL; RetL3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997: U07726.
PR 10-APR-1997: US-017427.
PR 08-MAY-1996: US-017427.
PR 07-JUN-1996: US-019300.
PR 16-JUL-1996: US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
PI WPI: 98-018431/02.
DR N-PSDB: V00251.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2: Page 85-86; 113pp; English.
CC This amino acid sequence comprises human Ret ligand (RetL) RetL3,
CC deduced from cDNA clones (see V00251) isolated from a adult heart
CC and spinal cord libraries. Rat and human RetL1, human RetL2 and
CC mouse RetL3 sequences (see W37457-62) are also claimed. Human
CC RetL3 is 34.3% identical to human RetL1, 34.9% identical to human
CC RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key
CC component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
CC cells transfected or transfected with these vectors are claimed, as
CC well as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue.
CC Particularly kidney or neural tissue. Typical applications are:

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CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.

SO Sequence 400 AA.

Query Match 44.5%; Score 931; DB 28; Length 400;
 Best Local Similarity 36.4%; Pred. No. 1,296-80;
 Matches 142; Conservative 43; Mismatches 185; Indels 20; Gaps 14;

Db 18 ||||ppppllaagdpplteestrlmsclqarrkcgadptcsaayhnlscscslst-rlp 76
 15 LXTLXSLXXPLXKXSSXXKXKXDXVAXXKXAEKXSCXXXTTLQCKXAGKXKXKX 74
 Db 77 seepvpadcleaaqqlnsllgcmehrmkngvacldlyvtvtrarslgnylevdepy 136
 75 XXXXAXXEXCXAXEXLXSSLYDCRCRGMKEXXCLXITWSXKXKXKXKXLEKSPY 134
 Db 137 edtytsk-p--wkm-nl-sk1--nm1kpd-sdlclkfam1clndkcdrlrkaygeac-- 186
 135 EXPVTSRLSDIFRXXSXXSXXKXKXKXKXKXCDAAKACLNDCXKRLSAYIXKXKX 194
 Db 187 --sgp-hqgrhvcrlqlltfefkaeapaglllpcapndgceerrnrlapnca1p 243
 195 XXXSXERCNRRKCHALRQFDFKVPXHXHYGMLFCSCXXDXACXERRRQRTXPSCSYEX 254
 Db 244 va-pncldlrrlcfedp1crsrlvdfqchbmdllgt-categ-srclraylgltgntam 300
 255 XEPPCCLDRSKCRIDXLCSRHLADFXTNCPXKXKXKXKXKXKXKXKXKXKXKX 314
 Db 301 tnfysnvt--valscrcrgsgnlgeecemlegfshnpclteaiaakmrfhaqlsfq 358
 315 TPNVDSXXTXVAPWCXRGSGNXXECCERFLXXFPXNPLXNAIQAFGNGXVXXSQ 374
 Db 359 dwpbptfavmahqenpavirpqpwp1sf 388
 375 XXXPXXXTX-AXXXXXXVXXPPXKXKX 403

RESULT 10
 ID W37465 standard; Protein: 346 AA.
 AC W37465;

DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand, RetL3 partial sequence.
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00256.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells

PS Disclosure: Page 73-74; 113pp; English.
 CC This polypeptide comprises a partial sequence of mouse Ret ligand
 CC RetL3, deduced from EST AA050083 cDNA (see V00256). A full-length
 CC mouse RetL3 sequence (see W37465) was also obtained. Rat, mouse
 CC and human RetL3, RetL2 and RetL3 cDNA sequences (see V00245-51) and
 CC in methods for promoting cell growth and improving survival of
 CC cells, especially renal or neural cells.

SO Sequence 346 AA.

Query Match 41.2%; Score 861; DB 28; Length 346;
 Best Local Similarity 45.2%; Pred. No. 1,356-73;
 Matches 127; Conservative 29; Mismatches 107; Indels 18; Gaps 12;

Db 31 dcleaaeqnlrnsllldcchrmkngvacldlyvtvtrarslgnylevdepydvtvsk- 76
 83 ECKXAXEXLXSSLYDCRCRGMKEXXCLXITWSXKXKXKXKXKXKXKXKXKX 142
 Db 90 p--wkm-nl-sk1--nm1kpd-sdlclkfam1clndkcdrlrkaygeac----sg1- 136
 143 SDIFRXXSXXSXXKXKXKXKXKXKXCDAAKACLNDCXKRLSAYIXKXKXKXKX 194
 Db 138 qh1clqqlsfefkaeapaglllpcapndgceerrnrlapnca1p 243
 203 NRRKCHALRQFDFKVPXHXHYGMLFCSCXXDXACXERRRQRTXPSCSYEXEPPC 314
 Db 197 lrsfcrdplcrsrlvdfqchbmdllgt-categ-srclraylgltgntam 300
 263 LRSXCRIDXLCSRHLADFXTNCPXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 314
 Db 255 ntt--valscrcrgsgnlgeecemlegfshnpclteaiaakmrfhaqlsfq 358
 323 XTXXVAPWCXRGSGNXXECCERFLXXFPXNPLXNAIQAFGNGXVXXSQ 374

RESULT 11
 ID W37462 standard; Protein: 315 AA.
 AC W37462;

DT 21-MAY-1998 (first entry)
 DE Human Ret ligand, RetL3 partial sequence.
 KW Human Ret ligand; RetL; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00250.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2; Page 81-82; 113pp; English.
 CC This amino acid sequence comprises a human Ret ligand (RetL) RetL3
 CC partial polypeptide sequence, deduced from a partial clone (see
 CC V00250) isolated from a human adult heart cDNA library; a
 CC full-length RetL3 sequence (see W37463) is also claimed, as well
 CC as rat and human RetL1, human RetL2 and mouse RetL3 sequences
 CC (see W37455-61). Ret ligand is a key component of the Ret
 CC signalling pathway that specifically interacts with Ret receptor
 CC protein, triggering Ret dimerisation and/or autophosphorylation of

CC the Ret tyrosine kinase domain. Vectors containing ret3 DNA and
 CC prokaryotic or eukaryotic host cells transformed or transfected
 CC with these vectors are claimed, as well as a method for production
 CC of Ret3. Its soluble variants and fusion proteins with a toxin,
 CC imageable compound or radionuclide. Ret3, optionally when
 CC expressed from vectors in vivo, is used to promote growth of new
 CC tissue and survival of damaged tissue, particularly kidney or
 CC neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neuron disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 315 AA;

Query Match 38.2%; Score 799; DB 28; Length 315;
 Best Local Similarity 40.1%; Pred. No. 2,81e-67;

Matches 126; Conservative 34; Mismatches 135; Indels 19; Gaps 13;

DB 8 lrrssllgcmchrnmknqvacldlyvtvharalgnvldvspyedvtvk-p-wkm-n 63
 OY 91 LKXSSLYDCRCKRGMKEXXCLXVWSXHXLLXGXGXXLEXPVTSRLSDIFRXXS 150
 DB 64 l-skl--nmklkpd-sdclclfamclctlnkdcl-lrkaygac-----sgp-hcgrhncrlq 114
 OY 151 XNXXXXXXDXNXXXXXKXNCLDAARACNLDXCKRLRSAYIXXCCXXSXXERCNRCHKA 210
 DB 115 llffekaeephaqglllpcapndrgcgrrrntlapncalpvpa-pnclelrrlcsd 173
 OY 211 LRQFFKVPKXHXHYGMFCSCXXDXACXERRQITXPCSYEXXEXKPNCLDRSKCRD 270
 DB 174 plcrsrllvdfqthcnpmdllgt-cateq-srclrayllgltamcpnfsvnvt--val 229
 OY 271 XLCRSRLADFXTCXPRXRXRXTCXAXNXXCLAXYGLIGTMYTNPVDSXXTXVAP 330
 DB 230 sctcrgsgnlqecemlegffshnpcltealeakmrfhsqllsqdphnftfamaqnena 289
 OY 331 WCCRGSGNXXECCERFLXXFXNPNCLXNAIQFNGXDVXMQXPPXXXTX-AAxxxx 389
 DB 290 pavrpqwpwpslfs 303
 OY 390 XRYXXXPLXXXXS 403

RESULT 12
 ID R94563 standard; Protein: 1810 AA.
 AC R94563;
 DT 21-JUN-1996 (first entry)
 DE Chicken cytotoxicin.
 KW Cytotoxicin; neuron; neurite; cell attachment; cell elongation;
 KW fibronectin.
 OS Gallus sp.
 FH Key
 FT region location/Qualifiers
 FT 1..591
 FT /note= "Egf-like repeat region"
 FT 592..773
 FT /note= "fibronectin type III repeats I-II"
 FT 774..864
 FT /note= "fibronectin type III repeat III"
 FT 865..956
 FT /note= "fibronectin type III repeat IV"
 FT 957..1044
 FT /note= "fibronectin type III repeat V"
 FT 1318..1398
 FT /note= "fibronectin type III repeat VI"
 FT 1045..1317
 FT /note= "alternatively spliced fibronectin type
 FT III repeat VavDvc"
 FT 1132..1569
 FT region

FT /note= "fibronectin type III repeats VII and
 FT VIII (lacking 13 N-terminal amino acids)"
 FT 1318..1398
 FT /note= "fibronectin type III repeats III-VI"
 FT 1570..1810
 FT /note= "fibronogen domain plus fibronectin type
 FT III repeat VIII N-terminals"
 PN W09608513-A1.
 PD 21-MAR-1996.
 PF 14-SEP-1995; 011684.
 PR 16-SEP-1994; US-308359.
 PA (SCRI) SCRIPS RES INST.
 PI Grossin KL, Phillips G, Prieto AL;
 DR MPI: 96-179904/18.
 DR N-PSDB; T14548.
 PT Cytotoxicin polypeptide(s), derivs. and antibodies - capable of
 PT stimulating neuronal cell attachment, neurite out-growth and cell
 PT elongation
 PS Claim 9; Page 118-126; 159pp; English.
 CC Chicken cytotoxicin (R94563) and human cytotoxicin (R94562) are
 CC multidomain extracellular matrix proteins capable of stimulating
 CC neuronal cell attachment, neurite outgrowth and cell elongation.
 CC The cytotoxicins, or functional portions of them (see R94564-69),
 CC can be obtd. by expression of encoding DNA (see T14548 and
 CC (T14547) in host cells, e.g. as GST fusion proteins in Escherichia
 CC coli. They have therapeutic and diagnostic applns. and can be
 CC used to raise antibodies.
 CC Sequence 1810 AA;

Query Match 4.6%; Score 96; DB 16; Length 1810;
 Best Local Similarity 24.3%; Pred. No. 7.44e+00;
 Matches 25; Conservative 18; Mismatches 49; Indels 11; Gaps

DB 185 pncs-epacpncln-rglcvrakclceegfgedsgarcpdcndggkcvdgv-cvcl 241
 OY 248 PCSYEXXEXXPNCLDRXSC-RTDXLCRSRLA--D-FXTNCKPXXRXHXKXAXNXXCL 303
 DB 242 egyptgdcgeelcph--gcsghgrcvggrcvche-gfgedcn 281
 OY 304 XAYXGLI-GTXMTPNVVDSXTXXXVAPWCXCRGSGNXXECC 345

RESULT 13
 ID R56166 standard; Protein: 383 AA.
 AC R56166;
 DT 26-JAN-1995 (first entry)
 DE Neuroendocrine tumor dlk.
 KW Dlk; neuroendocrine tumor; monoclonal antibody.
 OS Homo sapiens.
 FH Key
 FT peptide location/Qualifiers
 FT 1..23
 FT /label= Sig_peptide
 FT 62
 FT /label= N-myristylation_site
 FT 72
 FT /label= N-myristylation_site
 FT 100
 FT /label= N-glycosylation_site
 FT 101
 FT /label= N-myristylation_site
 FT 109
 FT /label= N-myristylation_site
 FT 120
 FT /label= protein-kinase-C-phosphorylation_site
 FT 187
 FT /label= hydroxylation_site
 FT 288
 FT /label= protein-kinase-C-phosphorylation_site
 FT 302
 FT /label= protein-kinase-C-phosphorylation_site
 FT 312
 FT /label= N-myristylation_site
 FT 312
 FT /label= N-myristylation_site
 PN W09413701-A.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Mar 8 15:04:28 1999; MasPar time 23.89 Seconds
Tabular output not generated.
766,704 Million cell updates/sec

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Title: >US-08-866-354-44
Description: (1-489) from US08866354.rep
Perfect Score: 2092
Sequence: 1 XXXXXXXXXXXXXLTWS.....PYLMTLTXLXXLXXLXLETS 489

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Scoring table: PAM 150

Searched: 116738 seqs, 37463448 residues

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Post-processing: Minimum Match 08
                  Listing first 45 summaries
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Database: plr58

Statistics: Mean 42.322; Variance 73.547; scale 0.575

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	976	46.7	397	2	JE0082	GPI-linked receptor -	3.04e-196
2	108	5.2	493	2	JC5621	epidermal growth fact	1.82e-03
3	109	5.2	2524	2	A35844	Notch protein - Affic	1.26e-03
4	108	5.2	3002	2	A47221	fibrillin 1 precursor	1.82e-03
5	107	5.1	2871	2	A55567	fibrillin I - bovine	2.62e-03
6	105	5.0	2871	2	A55564	fibrillin-1 precursor	5.38e-03
7	96	4.6	387	2	I38448	extracellular protein	1.25e-01
8	96	4.6	1810	2	A52230	tenascin precursor	1.25e-01
9	96	4.6	570	2	A48836	fibropellin C precurs	2.44e-01
10	94	4.5	879	1	ORR1LD	LDL receptor precursor	2.44e-01
11	95	4.5	1232	2	D64413	cobalamin blosynthesis	1.75e-01
12	94	4.5	1700	2	S08167	Babbin1 ring 3 prote	2.44e-01
13	95	4.5	2531	2	A46019	gene Notch-1 protein	1.75e-01
14	94	4.5	2555	2	A40043	notch protein homolog	2.44e-01
15	92	4.4	259	2	S44735	revel antigen 1 - hum	4.74e-01
16	92	4.4	260	2	A44349	revel antigen 1 - hmo	4.74e-01
17	92	4.4	383	2	B45484	delta-1-like dlx homeot	4.74e-01
18	92	4.4	383	2	S53716	homeotic protein dlx	4.74e-01
19	93	4.4	469	2	A56918	farnesoid x-activated	4.74e-01
20	92	4.4	2703	2	A24420	notch protein - fruit	3.41e-01
21	92	4.4	2907	2	A57278	fibrillin-2 precursor	4.74e-01
22	92	4.4	2918	2	A34105	fibrillin-2 precursor	4.74e-01
23	89	4.3	200	2	A26633	neurogenic repetitive	1.26e-00

45	86	4.1	972	2	A0363	glycoprotein GP330, r	1.25e+00
44	86	4.1	886	2	A57172	probable hormone rece	3.25e+00
43	86	4.1	832	2	A11246	neurogenic protein De	3.25e+00
42	86	4.1	370	2	BH3306	Dnrf - Streptococci p	3.25e+00
41	86	4.2	3069	2	HT0656	probable fas protein	1.73e+00
40	88	4.2	2139	2	A57263	crumbs protein - fru1	1.73e+00
39	87	4.2	1251	2	A57293	latent transforming r	1.38e+00
38	88	4.2	1203	2	A9175	Motch B protein - mou	1.73e+00
37	87	4.2	903	2	SC0257	meltin alpha - mouse	2.38e+00
36	87	4.2	385	2	SS3718	homeotic protein dlf	2.38e+00
35	87	4.2	385	2	B56378	neurogenic repetitive	1.73e+00
34	88	4.2	293	2	B26637	cadherin-related tumo	1.26e+00
33	89	4.3	5147	1	IFP7M	hypothetical protein	9.17e-01
32	90	4.3	3051	2	A82373	masking protein precu	1.25e+00
31	89	4.3	1712	2	A82821	IDL receptor precursor	1.25e+00
30	89	4.3	854	1	ONHYD	monocytic surface anti	6.59e-01
29	91	4.3	826	2	AC0385	coagulation factor XI	1.26e+00
28	89	4.3	603	2	S28941	dopamine receptor pro	1.26e+00
27	89	4.3	511	2	S44275	Ybnc protein precursor	9.17e-01
26	90	4.3	427	2	D64813	dopamine D1-like rece	1.25e+00
25	89	4.3	385	2	SO9868	hypothetical protein	1.25e+00
24	89	4.3	249	2	S08780	dopamine D1-like rece	1.25e+00
23	89	4.3	285	2	SO8780	dopamine D1-like rece	1.25e+00
22	89	4.3	427	2	D64813	Ybnc protein precursor	9.17e-01
21	89	4.3	511	2	S44275	dopamine receptor pro	1.26e+00
20	89	4.3	603	2	S28941	coagulation factor XI	1.26e+00
19	91	4.3	826	2	AC0385	monocytic surface anti	6.59e-01
18	89	4.3	854	1	ONHYD	IDL receptor precursor	1.25e+00
17	89	4.3	1712	2	A82821	masking protein precu	1.25e+00
16	90	4.3	3051	2	A82373	masking protein precu	1.25e+00
15	89	4.3	5147	1	IFP7M	cadherin-related tumo	1.26e+00
14	88	4.2	293	2	B26637	neurogenic repetitive	1.73e+00
13	87	4.2	385	2	B56378	neurogenic repetitive	1.73e+00
12	87	4.2	385	2	SS3718	homeotic protein dlf	2.38e+00
11	87	4.2	903	2	SC0257	meltin alpha - mouse	2.38e+00
10	88	4.2	1203	2	A9175	Motch B protein - mou	1.73e+00
9	87	4.2	1251	2	A57293	latent transforming r	1.38e+00
8	88	4.2	2139	2	A57263	crumbs protein - fru1	1.73e+00
7	88	4.2	3069	2	HT0656	probable fas protein	1.73e+00
6	86	4.1	370	2	BH3306	Dnrf - Streptococci p	3.25e+00
5	86	4.1	832	2	A11246	neurogenic protein De	3.25e+00
4	86	4.1	886	2	A57172	probable hormone rece	3.25e+00
3	86	4.1	972	2	A0363	glycoprotein GP330, r	3.25e+00

ALIGNMENTS

RESULT	1
ENTRY	JE0082.
TITLE	#type complete
ALTERNATE_NAMES	GPI-linked receptor - mouse
ORGANISM	#fomal_name Mus musculus #common_name house mouse
DATE	21-May-1998 #sequence_revision 29-May-1998 #text_change

ACCESSIONS
REFERENCE

#authors Nomoto, S.; Ito, S.; Yang, L.X.; Kinosh, K.
#journal Biochem. Biophys. Res. Commun. (1998) 244:849-853
#title Molecular cloning and expression analysis of Gfra1pha-3, a novel cDNA related to GDNFalpha and NTRalpha.

###MO

```
##residues      1-397 ##label NOM
##cross-references DDBJ:AB008833; NID:q2627159; PID:q2627160
COMMENT  This protein plays a distinct role in cell survival and
         differentiation.
```

FEATURE

1-25	#domain signal sequence	#status predicted	#label size
380-397	#region hydrophobic\		
92,145,306	#binding_site carbohydrate (Asn)	(covalent)	#status

SUMMARY

Query Match 46.78; Score 976; DB 2; Length 397;

Matches

Db 10 PLMLLLVLSWLPICAGNSLATENRFVNSCTQARKKCEANPCKAKAYOHIGSCTSL 66

25

```

Db      70 RPLPLEESAMSA-DCLEAAEQLRNSSLIDCRRMKHQATCLDIYWTVHPARSLGDIYI
      :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

```
Db      129 DVSPEEDVTISK-P--WKM-NL-SKL--NMLKPD-SDCLCKFAMLCCTLHDKCDRLRKAYG 180  
          :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
          :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

191

```

DB      |-----S61-KCQKHTC LQ LKRSFEFEAAEASHADG LBLDPCAPEDVAGCCENKRN1 IAPS 235
181     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0V 190 |XXXXXXXXXXERCNRRCHKALROFEDVPYBXHHXGMECSXXXXDAXCERRROTIXPS 249

```


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```

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on:      Mon Mar 8 15:07:33 1999;      MasPar time 36.57 Seconds
Tabular output not generated.              737.616 Million cell updates/sec

```

```
Title: >US-08-866-354-.44
Description: (1-489) from US08866354..pep
Perfect Score: 2092
Sequence: 1 XXXXXXXXXXXXXLTLMS.....PVLMLTXXXXLXXXLKXETS 488
```

Scoring table: PAM 150
Gap 11

```
Searched:      180763 segs, 55169189 residues
Post-processing: Minimum Match 0%
                  Listing first 45 summaries
```

1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_orignele
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 42.421; Variance 67.360; scale 0.630

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1800	86.0	464	11	035977	GIAL CELL LINE-DERIVE	0.00e+00
2	1768	84.5	464	4	015328	RET LIGAND 2.	0.00e+00
3	1768	84.5	464	4	015316	GIAL CELL LINE-DERIVE	0.00e+00
4	1762	84.2	468	11	035346	GNF RECEPTOR ALPHA.	0.00e+00
5	1728	82.6	463	11	035748	GNFR-ALPHA/TRNR1-DELT	0.00e+00
6	1711	81.8	463	11	035352	GNF RECEPTOR BETA.	0.00e+00
7	1695	81.0	465	4	043912	GPI-LINKED ANCHOR PROT	0.00e+00
8	1644	78.6	460	4	015507	RET LIGAND 1.	0.00e+00
9	1264	59.5	431	13	035118	GFR RECEPTOR ALPHA 4 P	1.79e-28
10	976	46.7	397	11	035118	GIAL CELL LINE DERIVE	6.99e-21
11	976	46.7	397	11	035125	GIAL CELL LINE-DERIVE	6.99e-21
12	976	46.7	397	11	053443	GIAL CELL LINE-DERIVE	6.99e-21
13	928	44.4	400	4	060609	GNF FAMILY RECEPTOR A	2.57e-22
14	108	5.2	493	11	035368	MEGF5.	6.96e-04
15	105	5.0	1523	11	083880	MUTANT FIBRILIN-1.	2.28e-02
16	105	5.0	3657	11	088840	COSMID C046E.	2.28e-02
17	97	4.6	192	5	001471	EXTRACELLULAR PROTEIN	4.80e-02
18	96	4.6	387	4	012805	NOTCH RECEPTOR PROTEIN	6.96e-02
19	97	4.6	752	13	042374	FIBRILIN-2 (FRAGMENT)	4.80e-02
20	96	4.6	1062	11	Q60789	FIBRILIN-2 (FRAGMENT)	6.96e-02

21	96	4.6	1810	13	075084	CYTOTACTIN 20KD PRECU	6.96e-07
22	95	4.5	739	4	075094	MEEF5 (FRAGMENT).	1.00e-07
23	95	4.5	1232	1	058318	HYPOTHEITICAL PROTEIN M	1.00e-07
24	94	4.5	1532	13	090994	190 KD TENASCIN PRECUR	1.45e-07
25	94	4.5	1698	5	034438	185 KDA SILK PROTEIN.	1.45e-07
26	94	4.5	1714	13	090995	200 KD TENASCIN PRECUR	1.45e-07
27	92	4.4	469	11	062735	FANESMOD X ACTIVATED	2.98e-07
28	93	4.4	733	5	025678	FIBRILLIN (FRAGMENT).	2.08e-07
29	92	4.4	1077	3	074853	POTATIVE CYSTEINE-RICH	2.98e-07
30	92	4.4	1127	5	094248	CODED FOR BY C. ELEGAN	2.98e-07
31	93	4.4	2531	5	016004	NORCH HOMOLOG.	2.98e-07
32	92	4.4	2533	5	027183	ALPHA-51D-IMMOBILIZATI	2.98e-07
33	92	4.4	2533	5	060589	ALPHA-51D-IMMOBILIZATI	2.98e-07
34	89	4.3	204	5	091208	COSMID F07C4.	8.61e-07
35	89	4.3	406	5	025059	FIBROPELLIN III (FRAGM	8.61e-07
36	91	4.3	596	2	048826	OXMALOCEPATE DECARBOXY	6.06e-07
37	91	4.3	660471	1	060487	MEMIONINE SYNTHASE RE	4.26e-07
38	90	4.3	767	5	020176	COSMID F18E9.	6.06e-07
39	89	4.3	1258	13	093520	REVERSE TRANSCRIPTASE.	8.61e-07
40	89	4.3	1704	5	094446	220 KDA SILK PROTEIN.	8.61e-07
41	89	4.3	1713	11	088349	LAMENT TGF BETA BINDIN	8.61e-07
42	91	4.3	1827	5	020535	SIMILARITY TO EGF-TYPE	4.26e-07
43	91	4.3	2543	5	090649	15SD SURFACE ANTIGEN.	4.26e-07
44	89	4.3	2653	5	025253	NORCH HOMOLOG SCALOPE	8.61e-07
45	91	4.3	3507	5	023587	CODED FOR BY C. ELEGAN	4.26e-07

ALIGNMENTS

ID	RESULT
AC	PRELIMINARY:
AD	PRT: 464 AA.
DT	035977;
DJ	01-JAN-1998 (TREMBREL, 05, CREATED)
DJ	01-JAN-1998 (TREMBREL, 05, LAST SEQUENCE UPDATE)
DJ	01-NOV-1998 (TREMBREL, 08, LAST ANNOTATION UPDATE)
DE	GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GN	GDNF-BETA OR RETL2.
OS	RATUS NORVEGICUS (RAT).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA
CC	SCURROGNATHI; MORIDAE; MORINAE; RATIOS.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	TRUMP M., RAYNSCHER C., IBANEZ C.F.;
RL	SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE-BRAIN/KIDNEY;
RX	MEDLINE: 97322356.
RA	SAITCOLA M., HESSION C.A., WORLEY D.S., CAMMILLO P., EHRENFELS C.
RA	WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITT A.,
RA	PERINSKY R.B., CAPE R.L.;
RT	"Glial cell line-derived neurotrophic factor-dependent RET activation"
RT	"can be mediated by two different cell-surface accessory proteins.";
RL	PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE-BRAIN/KIDNEY;
RA	SAITCOLA M., HESSION C.A., WORLEY D.S., CAMMILLO P., EHRENFELS C.,
RA	WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITT A.,
RA	PERINSKY R.B., CAPE R.L.;
RL	SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR	EMBL: AF005226; G232252; "-."
SO	EMBL: U09143; G2282024; "-."
SO	SEQUENCE 464 AA; 51668 MW; BA12BD11 CRC32;
Query Match 86.0%; Score 1800; DB 11; Length 464;	
Best Local Similarity 54.5%; Pied. No. 0.00e+00;	
Matches 250; Conservative 9; Mismatches 187; Indels 13; Gaps	
Dj	16 TLRSASPSSLQSELHGWRPOVDYCRANETCAAESNCSSRYRTLROCLAGRDNTML-- 73
Ig	11
Ig	17 TLSLSKPLSLXXSKKKKXXXXDCVKAXKXCALKXCSXYRFLRRQCAGKXXXXXXXX 76

Db 74 ---ANKCOALAEVLOESPLDRCRGMKKELOIYWSIHGLTEGEFEYASPYE- 129
 Oy 77 XXXAXXEXAXXEXLXXSSLYDCRCRGMKEXXCLXIYWSXHXHXXGXGXXLEASPYEX 136
 Db 130 PVTSLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDCKRLRSYSISICNREI 189
 Oy 137 PVTSLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDCKRLRSYSISICNREI 196
 Db 190 SPTERCNRKRCHALROFDFVPESEYTYRMLFCSCQ--DOACERRRQTLIPSCSYEDKE 247
 Oy 197 SXKRCNRKRCHALROFDFVPESEYTYRMLFCSCQ--DOACERRRQTLIPSCSYEDKE 256
 Db 248 KPNCLDLRGVCTDHLCSRLADFHANCRASTYQITSCPADNYOACLSYAGMIGFDMT 307
 Oy 257 XPNCLDLRGVCTDHLCSRLADFHANCRASTYQITSCPADNYOACLSYAGMIGFDMT 316
 Db 308 NYVDSSTGTIVSPWCNCRSGNMECEKFLRDFTEPCLRNAIOAFNGXDVMXSOXX 367
 Oy 317 NYVDSSTGTIVSPWCNCRSGNMECEKFLRDFTEPCLRNAIOAFNGXDVMXSOXX 376
 Db 368 PSFGATQAP-----RVEKTPSLPDDLSSTSLGTSVITTCSTVOEQGLKANNKELSMCF 422
 Oy 377 PAXXXXTAXXXXXRXVXXXPXLLXXXSXGXXXTYVXXCXGXQXQXLLKXNXXSXGXXCX 436
 Db 423 TELTNIIPGSKVKIKLNSGSRARLSALTALPLMLT 461
 Oy 437 XXXXXXXXXXXXXXXXXXXXXSXXLXLLPLVLM 475

RESULT 2
 ID 015328 PRELIMINARY: PRT: 464 AA.
 AC 015328;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE RET LIGAND 2.
 GN RETL2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 9732356.
 RA SANCOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA MAULIS L., ROBINSON S., JAMORSKI G., WEI H., TITARD R., WHITTY A.,
 RA PEPIUSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins".
 RL PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 DR EMBL: U97145; G2282028; -
 SO SEQUENCE 464 AA; 51543 MW; 288ABBD8 CRC32;

Query Match 84.5%; Score 1768; DB 4; Length 464;
 Best Local Similarity 53.3%; Pred. No. 0.00e+00;
 Matches 244; Conservative 14; Mismatches 187; Indels 13; Gaps 4;

Db 16 TLRLASPSLOGPELHGMRPVDCVARNELCAESNCSKRITRLROCLAGRDNTML-- 73
 Oy 17 TLRLASPSLOGPELHGMRPVDCVARNELCAESNCSKRITRLROCLAGRDNTML-- 76
 Db 74 ---ANKCOALAEVLOESPLDRCRGMKKELOIYWSIHGLTEGEFEYASPYE- 129
 Oy 77 XXXAXXEXAXXEXLXXSSLYDCRCRGMKEXXCLXIYWSXHXHXXGXGXXLEASPYEX 136
 Db 130 PVTSLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDCKRLRSYSISICNREI 189
 Oy 137 PVTSLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDCKRLRSYSISICNREI 196
 Db 190 SPTERCNRKRCHALROFDFVPESEYTYRMLFCSCQ--DOACERRRQTLIPSCSYEDKE 247
 Oy 197 SXKRCNRKRCHALROFDFVPESEYTYRMLFCSCQ--DOACERRRQTLIPSCSYEDKE 256

Db 248 KPNCLDLRGVCTDHLCSRLADFHANCRASTYQITSCPADNYOACLSYAGMIGFDMT 307
 Oy 257 XPNCLDLRGVCTDHLCSRLADFHANCRASTYQITSCPADNYOACLSYAGMIGFDMT 316
 Db 308 NYVDSSTGTIVSPWCNCRSGNMECEKFLRDFTEPCLRNAIOAFNGXDVMXSOXX 367
 Oy 317 NYVDSSTGTIVSPWCNCRSGNMECEKFLRDFTEPCLRNAIOAFNGXDVMXSOXX 376
 Db 368 PSFGATQAP-----RVEKTPSLPDDLSSTSLGTSVITTCSTVOEQGLKANNKELSMCF 422
 Oy 377 PAXXXXTAXXXXXRXVXXXPXLLXXXSXGXXXTYVXXCXGXQXQXLLKXNXXSXGXXCX 436
 Db 423 TELTNIIPGSKVKIKLNSGSRARLSALTALPLVLM 460
 Oy 437 XXXXXXXXXXXXXXXXXXXXXSXXLXLLPLVLM 474

RESULT 3
 ID 015316 PRELIMINARY: PRT: 464 AA.
 AC 015316;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
 GN GDNFR-BETA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FETAL BRAIN;
 RA MARTIOVANA K., SUVANTO P., HORELLI-KUTTUEN N., LINDAHL M.,
 RA MOSHAKOV M., AIRAKSIJEN M.S., PALOTIE A., SARIOLA H., SAARMA M.,
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U93703; G2228737; -
 SO SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;

Query Match 84.5%; Score 1768; DB 4; Length 464;
 Best Local Similarity 53.3%; Pred. No. 0.00e+00;
 Matches 244; Conservative 14; Mismatches 187; Indels 13; Gaps 4;

Db 16 TLRLASPSLOGPELHGMRPVDCVARNELCAESNCSKRITRLROCLAGRDNTML-- 73
 Oy 17 TLRLASPSLOGPELHGMRPVDCVARNELCAESNCSKRITRLROCLAGRDNTML-- 76
 Db 74 ---ANKCOALAEVLOESPLDRCRGMKKELOIYWSIHGLTEGEFEYASPYE- 129
 Oy 77 XXXAXXEXAXXEXLXXSSLYDCRCRGMKEXXCLXIYWSXHXHXXGXGXXLEASPYEX 136
 Db 130 PVTSLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDCKRLRSYSISICNREI 189
 Oy 137 PVTSLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDCKRLRSYSISICNREI 196
 Db 190 SPTERCNRKRCHALROFDFVPESEYTYRMLFCSCQ--DOACERRRQTLIPSCSYEDKE 247
 Oy 197 SXKRCNRKRCHALROFDFVPESEYTYRMLFCSCQ--DOACERRRQTLIPSCSYEDKE 256
 Db 248 KPNCLDLRGVCTDHLCSRLADFHANCRASTYQITSCPADNYOACLSYAGMIGFDMT 307
 Oy 257 XPNCLDLRGVCTDHLCSRLADFHANCRASTYQITSCPADNYOACLSYAGMIGFDMT 316
 Db 308 NYVDSSTGTIVSPWCNCRSGNMECEKFLRDFTEPCLRNAIOAFNGXDVMXSOXX 367
 Oy 317 NYVDSSTGTIVSPWCNCRSGNMECEKFLRDFTEPCLRNAIOAFNGXDVMXSOXX 376
 Db 368 PSFGATQAP-----RVEKTPSLPDDLSSTSLGTSVITTCSTVOEQGLKANNKELSMCF 422
 Oy 377 PAXXXXTAXXXXXRXVXXXPXLLXXXSXGXXXTYVXXCXGXQXQXLLKXNXXSXGXXCX 436
 Db 423 TELTNIIPGSKVKIKLNSGSRARLSALTALVLM 460
 Oy 437 XXXXXXXXXXXXXXXXXXXXXSXXLXLLPLVLM 474

RESULT 4 PRELIMINARY; PRT: 468 AA.

ID 035246

AC 035246

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE GENE RECEPTOR ALPHA.

DE GDNFR-ALPHA.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;

OC SCIUROGNATHI; MORIDAE; MORINAE; MUS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57; TISSUE-LIVER;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL NEUROREPORT 9:0-0(0001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-C57; TISSUE-LIVER;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF014117; G2624961; -

SO SEQUENCE 468 AA; 51751 MW; AFDCE6A1 CRC32;

Query Match 84.2%; Score 1762; DB 11; Length 468;

Best Local Similarity 49.7%; Pred. No. 0.00e+00;

Matches 236; Conservative 19; Mismatches 211; Indels 9; Gaps 8;

Db 3 LATLYFLPLDLMSAEVSGGDRDCVAKASDCLKEGSCSTKYRTLROCVAGKETNFSL 62

15 LXTLSLXPLXLLXSSXXXXXXDCVAXXCKAEKXGXXRTLRQAGAGXXXXXX 74

Db 63 TSGLEAKDECRSAMEALKOKSLYNCRCRGMKREKNCILRYMSYSLQ-GNDLEDSPY 121

75 XXXXXAXXECXAXEXLXSSSLYDCRCKGMKREKXCLXIYWSXHXLLXGXHXLESPY 134

Db 122 E-PVNSRLSDIFRAVPFISVDFQOVHISKGNCLDAKACNLDTCKRYRSAYITPCTT 180

135 EXPVTSRLSDIFRAXXSSXXXXXXKXNCLDAKACNLDTCKRLRSAYITXXCX 194

Db 181 SMSN-EVCNRRKCHKALROFEDKVPKHSYGMFCSCR--DIACERRRQTIYVCSYEE 237

195 XXSXEXECNRRKCHKALROFEDKVPKHSYGMFCSCXKXKACERRRQTIYVCSYEX 254

Db 238 RERNCLNLDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGTYM 297

255 XEXPNCLDLRSXCRTDYLCSRLADFTNCPXKXRXXTXCAKXNYXXCLXAYXGLIGTYM 314

Db 298 TPNTIDSS-SLS-VAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 355

315 TPNTVDSXKTXVAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 374

Db 356 PAPVOTTTATTTAATFRKNRP-LGPAGSENEIP-THVLPCCANLQAOGLKSNVSGSTHL 413

375 XXPXXXXXKTXVAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 434

Db 414 CLSDNDYGDGLAGASSHTTKSMAAPPSGSLSPVMTALALLSVSLAETS 468

435 CXXXXXXKTXVAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 489

RESULT 5 PRELIMINARY; PRT: 463 AA.

ID 035748

AC 035748

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE GDNFR-ALPHA/TRNKI-DELTA PROTEIN.

OS RATUUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;

OC SCIUROGNATHI; MORIDAE; MORINAE; RATUUS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-HANNOVER;

RA ZHONG J., ANNIEN M., HEUMANN R.;

RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF002072; E1134274; -

SO SEQUENCE 463 AA; 51032 MW; 93277991 CRC32;

Query Match 82.6%; Score 1728; DB 11; Length 463;

Best Local Similarity 50.7%; Pred. No. 0.00e+00;

Matches 241; Conservative 12; Mismatches 208; Indels 14; Gaps 10;

Db 3 LATLYFLPLDLMSAEVSGGDRDCVAKASDCLKEGSCSTKYRTLROCVAGKETNFSL 62

15 LXTLSLXPLXLLXSSXXXXXXDCVAXXCKAEKXGXXRTLRQAGAGXXXXXX 74

Db 63 TSGLEAKDECRSAMEALKOKSLYNCRCRGMKREKNCILRYMSYSLQ-GNDLEDSPY 121

75 XXXXXAXXECXAXEXLXSSSLYDCRCKGMKREKXCLXIYWSXHXLLXGXHXLESPY 134

Db 122 E-PVNSRLSDIFRAVPFISVDFQOVHISKGNCLDAKACNLDTCKRYRSAYITPCTT 180

135 EXPVTSRLSDIFRAXXSSXXXXXXKXNCLDAKACNLDTCKRLRSAYITXXCX 194

Db 176 SMSN-EVCNRRKCHKALROFEDKVPKHSYGMFCSCR--DIACERRRQTIYVCSYEE 237

195 XXSXEXECNRRKCHKALROFEDKVPKHSYGMFCSCXKXKACERRRQTIYVCSYEX 254

Db 238 RERNCLNLDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGTYM 297

255 XEXPNCLDLRSXCRTDYLCSRLADFTNCPXKXRXXTXCAKXNYXXCLXAYXGLIGTYM 314

Db 293 TPNTVDS-SLS-VAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 350

315 TPNTVDSXKTXVAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 374

Db 351 PAPVOTTTATTTAATFRKNRP-LGPAGSENEIP-THVLPCCANLQAOGLKSNVSGSTHL 408

375 XXPXXXXXKTXVAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 434

Db 409 CLSDSDYGDGLAGASSHTTKSMAAPPSGSLSPVMTALALLSVSLAETS 463

435 CXXXXXXKTXVAPMDCSNGNLEDCIKFLNFNDNTCLNNAIOAFNGSDVTMMQ 489

RESULT 6 PRELIMINARY; PRT: 463 AA.

ID 035252

AC 035252

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE GENE RECEPTOR BETA.

DE GDNFR-BETA.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;

OC SCIUROGNATHI; MORIDAE; MORINAE; MUS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL NEUROREPORT 9:0-0(0001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-C57;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF015172; G2624963; -

SO SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;

Query Match 81.8%; Score 1711; DB 11; Length 463;

Best Local Similarity 49.7%; Pred. No. 0.00e+00;

Matches 236; Conservative 19; Mismatches 206; Indels 14; Gaps 10;

Db 3 LATLYFLPLDLMSAEVSGGDRDCVAKASDCLKEGSCSTKYRTLROCVAGKETNFSL 62

Oy		15	LATLSTLXKPLXLXXXXXXXRXDXCQVAXXXXCAXEKKCSXXHTYLQCAGAXXNNXX	74
Dd		63	TSGLEAKBECBSAMEALKQKSLYNCRCRGMKEKNCLRIYMSQTSLQ-GNDLEDSPY	121
Oy		75	XXXXXXXXXXECCXAAXEXLXSLSLYDCRCRKRMKREXXCLXIYMSHXHLLXGXHLENSPY	134
Dd		122	E-PVNSRLSDIEFRVAVPTLSV---EHIS--KGNNCLDAAACNLDDTCRRKSAYITPCTT	175
Oy		135	EXPVTSRLSDIFRXXSXSSXXXDXXXXXXSNCKCDPAAACVLNDCXCKRLSAVIYXCXX	194
Dd		176	SMSN-EVCNRRKCHKALROEFEDVPKAPHSYGMLFSCSR--DVACTERRÖTIIVPCSYEE	232
Oy		195	XSXSERCNRRKCHKALROEFEDVPKPHXHGMLFCGCCAAXXDACERRÖTIIXSCSEX	254
Dd		223	RERNCLNLDOSCTWNTICSRSLADEFTTCOPEPSRSVNCLEKENYADCLLAYSGLIETVM	292
Oy		255	XEPNPCDLRSXCRTDILCRSLADEFYTNCPXXRXXTJCYAXNYXCCLMAYXGLIGTM	314
Dd		293	TPNYIDS-SLS-VAPMCDOSNGNDLECILFLNEFKNTCLKAIAFGNSDYTIMQ	350
Oy		315	TPNVYDSXTHYXXVAPMCXGRGSGNXXEBCERFLXXFXFNPLNAIOPANGXDVMQS	374
Dd		351	PAPPQTTATTATTTAFIRKKRP-LGPAGSENEIP-THVLPSCANLOAKLSNYSGSTHL	408
Oy		375	XXPXXXXTXAXXXXXXXVXXXPYLXXXXXSSXXXXTYAXXXCXQOXLXXNXSXXXXX	434
Dd		409	CLSDNDYGKDGLAGASSHITTKSMAPPCSGLSLPVVVFTLAALLSVSLAETS	463
Oy		435	CXXXXXXXSXXXXXXXXXXXXXSXXSXLLXLPVLTGLTXXXXLXXLXETS	489
RESULT		7		
ID	043912	PRELIMINARY:	PRT:	465 AA.
AC	043912;			
DT	01-JUN-1998 (TREMBLREL, 06, CREATED)			
DT	01-JUN-1998 (TREMBLREL, 06, LAST SEQUENCE UPDATE)			
DT	01-AUG-1998 (TREMBLREL, 07, LAST ANNOTATION UPDATE)			
DE	GPI-LINKED ANCHOR PROTEIN.			
GN	HOMO SAPIENS (HUMAN).			
OC	EUFAROTI; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES			
CC	CARNARIINI; HOMINIDAE; HOMO.			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RA	ANRIST M., JING S., BULK S., BENTLEY K., NATLASAMY S., HALUSKA M.,			
RA	FOX G.M., CHAKRAVARTI A.;			
RL	GENOMICS 0:0-0(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;			
RA	SHEFFELINE S.E., KHORANA S., SCHULTZ P.N., HUANG E., THOBÉ N., HU Z.J.,			
RA	FOX G.M., JING S., CORE G.J., GAGEL R.F.;			
RL	HUM. GENET. 0:0-0(1998)			
DR	EMBL: AF038420; G2921545; -			
DR	EMBL: AF038411; G2921545; JOINED.			
DR	EMBL: AF038412; G2921545; JOINED.			
DR	EMBL: AF038413; G2921545; JOINED.			
DR	EMBL: AF038414; G2921545; JOINED.			
DR	EMBL: AF038415; G2921545; JOINED.			
DR	EMBL: AF038416; G2921545; JOINED.			
DR	EMBL: AF038417; G2921545; JOINED.			
DR	EMBL: AF038418; G2921545; JOINED.			
DR	EMBL: AF038419; G2921545; JOINED.			
DR	EMBL: AF042080; G2801557; -			
DR	EMBL: AF038421; G2921532; -			
DR	EMBL: AF038999; G306783; -			
DR	EMBL: AF058990; G306783; JOINED.			
DR	EMBL: AF058991; G306783; JOINED.			
DR	EMBL: AF058992; G306783; JOINED.			
DR	EMBL: AF058993; G306783; JOINED.			
DR	EMBL: AF058994; G306783; JOINED.			
DR	EMBL: AF058995; G306783; JOINED.			

[illegible]

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RESULT      8      PRELIMINARY:      PRT:      460 AA.
ID      015507
AC      015507;
DT      01-JAN-1998 (TREMBLREL, 05, CREATED)
DT      01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
DT      01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
DE      RET LIGAND 1.
GN      HML.
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES
OC      CATARRHINI; HOMINIDAE; HOMO.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-KIDNEY:
RX      MEDLINE: 97322356.
RA      SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
RA      WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA      PEPINSKY R.B., CATE R.L.;
RT      "Glia1 cell line-derived neurotrophic factor-dependent RET activation
RT      can be mediated by two different cell-surface accessory proteins.";
RL      PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE-KIDNEY;
RA      SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
RA      WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA      PEPINSKY R.B., CATE R.L.;
RT      SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE-SUBSTANTIA NIGRA:

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